Transcriptional Intermediary Factor-2

Cross-Reference to Related Applications

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This application claims priority to U.S. Appl. No. 60/021,247, filed July 12, 1996, which is herein incorporated by reference.

Field of the Invention

The present invention relates to a nuclear receptor (NR) transcriptional mediator. More specifically, isolated nucleic acid molecules are provided encoding transcriptional intermediary factor-2 (TIF2). Recombinant methods for making TIF2 polypeptides are also provided as are screening methods for identifying agonists and antagonists of the activation function AF-2 of nuclear receptors, as well as TIF2 antibodies. Also provided are screening methods for identifying agonists and antagonists of TIF2 AD1 activation domain activity, as are provided screening methods for identifying agonists and antagonists of TIF2 AD2 activation domain activity.

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Background of the Invention

Activators that enhance the initiation of transcription by RNA polymerase B (II) are composed of at least two functional domains: a DNA binding domain and an activating domain (M. Ptashne, *Nature 335*:683-689 (1988); P.J. Mitchell *et al.*, *Science 245*:371-378 (1989)). These two domains are generally separable functional units and each can actually be interchanged with the complementary region of an unrelated activator, thereby creating functional chimeric activators (S. Green *et al.*, *Nature 325*:75-78 (1987)).

A number of structure-function analyses of eukaryotic transcriptional activators have been performed, focussing primarily on the yeast GAL4 and GCN4 proteins and on members of the nuclear receptor family. GAL4 and GCN4

proteins activate transcription by binding to specific upstream activation sequence, which have many of the characteristics of higher eukaryotic enhancer elements (K. Struhl, *Cell 49*:295-297 (1987)). The herpes simplex activator VP16 represents another type of activator, which activates transcription by binding to the DNA-bound octamer transcription factor rather than binding to the DNA directly (T. Gerster *et al.*, *Proc. Natl. Acad. Sci. USA 85*:6347-6351 (1988)).

The nuclear receptor family, which includes receptors for steroid hormones, thyroid hormones, vitamin D, and the vitamin A derivative retinoic acid, are also transcriptional enhancer factors which bind DNA directly in the presence of their cognate ligand by recognition of specific enhancer elements, *i.e.*, hormone- or ligand-responsive elements (R.M. Evans, *Cell 240*:889-895 (1988)). These cognate ligands tend to be small, hydrophobic molecules, including steroid hormones such as estrogen and progesterone, thyroid hormone, vitamin D, and various retinoids (S. Halachmi *et al.*, *Science 264*:1455-1458 (1994); Gronemeyer, H. and Laudet, V., *Protein Profile 2*:1173-1308 (1995)).

Despite their small size and apparently simple structure, however, the cognate ligands associated with NRs are known to elicit a wide range of physiological responses. Adrenal steroids for example, such as cortisol and aldosterone, widely influence body homeostasis, controlling glycogen and mineral metabolism, have widespread effects on the immune and nervous systems, and influence the growth and differentiation of cultured cells. The sex hormones (progesterone, estrogen and testosterone) provoke the development and determination of the embryonic reproductive system, masculinize/feminize the brain at birth, control reproduction and related behavior in adults and are responsible for development of secondary sex characteristics. Vitamin D is necessary for proper bone development and plays a critical role in calcium metabolism and bone differentiation. Significantly, aberrant production of these hormones has been associated with a broad spectrum of clinical disease, including cancer and similar pathologic conditions.

All NRs display a modular structure, with five to six distinct regions, termed A-F. The N-terminal A/B region contains the activation function AF-1, which can activate transcription constitutively. Region C encompasses the DNA binding domain (DBD), which recognizes cognate *cis*-acting elements. Region E contains the ligand-binding domain (LBD), a dimerization surface and the ligand-dependent transcriptional activation function AF-2 (reviewed in Mangelsdorft, D.J. *et al., Cell 83*:835-839 (1995a); Mangelsdorft & Evans, *Cell 83*:841-850 (1995b); Beato, M. *et al., Cell 83*:851-857 (1995); Gronemeyer & Laudet, "Transcription Factors 3: Nuclear Receptors", in *Protein Profile*, vol. 2, Academic Press (1995); Kastner, P. *et al., EMBO J. 11*:629-642 (1992); Chambon, P., *FASEB J 10*:940-954 (1996)).

Several classes of domains in activators are capable of mediating transcriptional activation. Yeast activators GAL4 and GCN4 and herpes simplex VP16 all contain activation domains that are composed of acidic stretches of amino acids, which may act by forming amphipathic α helices (I.A. Hope *et al., Cell 46*:885-894 (1986); J. Ma *et al., Cell 48*:847-853 (1987); E. Giniger *et al., Nature 330*:670-672 (1987); S.J. Triezenberg *et al., Genes Dev. 2*:718-729 (1988)). The activation functions of human Sp1 and CTF/NFI proteins contain glutamine- and proline-rich areas, respectively (A.J. Courey *et al., Cell 55*:887-898 (1988); N. Mermod *et al., Cell 58*:741-753 (1989)). Studies with steroid hormone receptors have shown that both the N-terminal A/B domain and the C-terminal hormone binding domain (HBD) contain transcription activation functions (AFs) (M.T. Bocquel *et al., Nucl. Acids Res., 17*:2581-2595 (1989); L. Tora *et al., Cell 59*:477-487 (1989)). The AFs of the human estrogen receptor (hER) do not contain stretches of acidic amino acids (S. Halachmi *et al., Science 264*:1455-1458 (1994)). Conversely, however, the human glucocorticoid receptor (hGR) contains two activation functions, τ-1 (located in the A/B domain) and τ-2 (located in the N-terminal region of the HBD), both of which are acidic (S.M. Hollenberg *et al., Cell 55*:899-906 (1988)).

From the results of studies on transcriptional interference/squelching between nuclear receptors and on homo- and heterosynergistic stimulation of initiation of transcription from minimal promoters by the activation functions present in hER (AF-1 and AF-2) and the acidic activator VP16, it has been proposed that AFs may activate transcription by interacting with different components of the basic initiation complex (Bocquel *et al., Nucl. Acids. Res. 17*:2581-2595 (1989); Meyer *et al., Cell 57*:433-442 (1989); L. Tora *et al., Cell 59*:477-487 (1989)). Studies of the transcriptional interference/squelching properties of AADs, hER AF-1 and hER AF-2, however, showed that both hER AF-1 and AF-2 can squelch acidic activators, such as VP16, but that the converse was not true, *i.e.*, AADs do not squelch hER AF-1 or AF-2. Moreover, hER AF-1 and AF-2, which are clearly distinguished by their synergistic properties, nevertheless squelch each other (D. Tasset *et al., Cell 62*:1177-1187 (1990)).

Based on these results, it was proposed that a string of transcriptional intermediary factors (TIFs) exists, interposed between enhancer factors and the basic transcriptional factors. For example, AF-1 and AF-2 have been suggested to contact the string of TIFs at functionally equivalent points, while AADs are believed to interact at an earlier point in the series (D. Tasset *et al., Cell 62*:1177-1187 (1990)).

Several putative coactivator TIFs for NR AF-2s have been characterized (see Chambon, P., *FASEB J 10*:940-954 (1996); Glass, C.K. *et al., Current Opin. Cell Biol. 9*:222-232 (1997); Horwitz, K.B. *et al., Mol. Endocrinol. 10:*1167-1177 (1996) for recent reviews). In particular, LeDouarin, B. *et al., EMBO J. 15:*6701-6715 (1996) have demonstrated that a 10-amino acid fragment of TIF1α is necessary and sufficient to mediate interaction with RXR in a ligand- and AF-2 integrity-dependent manner. Notably, within this TIF1α fragment, they identified a LxxLLL (SEQ ID NO:13) motif, termed NR box, whose integrity is required for interaction with nuclear receptors, and pointed out that this motif is conserved in several other putative coactivators (LeDouarin, B. *et al., EMBO J. 15:*6701-6715 (1996)) Whereas TIF1α and several other putative coactivators do not, or only

very poorly, stimulate transactivation by NRs in transiently transfected mammalian cells, the TIF2/SRC-1 family (Oñate, S.A. *et al., Science 270*:1354-1357 (1995); Voegel, J.J. *et al., EMBO J. 15*:3667-3675 (1996)), the CBP/p300 family (Kamei, Y. *et al., Cell 85*:403-414 (1996); Chakravarti, D. *et al., Nature 5*:99-103 (1996); Hanstein, B., *et al., Proc. Natl. Acad. Sci USA 93*:11540-11545 (1996); Smith, C.L. *et al., Proc. Natl. Acad. Sci. USA 93*:8884-8888 (1996); for recent reviews see Eckner, R. , *Biol. Chem. 377*:685-688 (1996); Janknecht &Hunter, *Current Biol. 6*:951-954 (1996b); Shikama, N. *et al., Trends in Cell Biol. 7*:230-236 (1997)) and the androgen receptor coactivator ARA70 (Yeh & Chang, *Proc. Natl. Acad. Sci. USA 93*:5517-5521 (1996)) have been unequivocally shown to enhance AF-2 activity.

In addition to binding NRs, CBP/p300 can also interact directly with SRC-1 (Kamei, Y. *et al., Cell 85*:403-414 (1996); Yao, T.P. *et al., Proc. Natl. Acad. Sci. USA 93*:10626-10631 (1996)) and both factors have been shown to exert histone acetyltransferase activity (Bannister & Kouzarides, *Nature 384*:641-643 (1996); Ogryzko, V.V. *et al., Cell 87*:953-959 (1996)). Moreover, CBP/p300 can recruit p/CAF which is itself a nuclear histone acetyltransferase (Yang, X.J. *et al., Nature 382*:319-324 (1996)). However, apart from interacting with coactivators in a ligand-dependent manner, NRs have also been shown to interact, often in a ligand-independent fashion, directly or indirectly with components of the transcriptional machinery, suds as TFIIB, TBP, TAFs, or TFIIH (Baniahmad *et al.*, (1993)); Jacq, X. *et al., Cell 79*:107-117 (1994); Schulman, IG. *et al., Mol. Cell. Biol. 16*:3807-3813 (1996); May, M. *et al., EMBO J. 15*:3093-3104 (1996); Mengus, G. *et al., Genes & Dev. 11*:1381-1395 (1997)).

Hong, H. *et al., Proc. Natl. Acad. Sci. USA 93*:4948-4952 (1996) originally described a partial cDNA of the mouse homologue of TIF2, named GRIP1, and recently reported the isolation of a full length GRIP1 cDNA (Hong, H. *et al., Mol. Cell. Biol.* 17:2735-2744 (1997)). Using the yeast *Saccharomyces cerevisiae* as a model system, they have shown that transcriptional activation by TR, RAR and RXR, could also be stimulated by GRIP1 coexpression, which

suggests that TIF2/GRIP1 could be a general coactivator for NRs (Hong, H. *et al., Mol. Cell. Biol.* 17:2735-2744 (1997)).

The overall picture emerging from multiple recent studies on the mechanisms by which nuclear receptors modulate target gene transcription involves three subsequent steps, (i) the ligand-induced transconformation of the NR LBD, which results in (ii) the dissociation of corepressors and formation of TIFs/coactivator complexes, which themselves (iii) through interaction with additional downstream factors (e.g., CBP, p300) modulate the acetylation status of core histones and, thus, chromatin condensation/decondensation. Histone acetylation on its own is, however, insufficient for transcription activation (Wong *et al.*, (1997)), and a simultaneous or subsequent fourth event comprises the direct and/or indirect recruitment of elements of the transcription machinery (e.g., TFIB, TBP, TAFs, TFIIH; Jacq, X. *et al., Cell 79*:107-117 (1994); Schulman, IG. *et al., Mol. Cell. Biol. 16*:3807-3813 (1996); May, M. *et al., EMBO J. 15*:3093-3104 (1996); Mengus, G. *et al., Genes & Dev. 11*:1381-1395 (1997)). Note that such interactions do not need to be ligand-dependent, if the primary function of the liganded LBD (AF-2) is to regulate DNA accessibility through chromatin remodeling. Indeed, several of the reported interactions between NRs and general transcription factors occur in a ligand-independent manner. Accordingly, there is a need in the art for the isolation and characterization of transcriptional intermediary factors.

Summary of the Invention

By screening 340,000 clones of a human placenta cDNA expression library with an estradiol-bound estrogen receptor probe, the present inventors have identified a cDNA clone containing the gene encoding transcriptional intermediary factor 2 (TIF2). By the invention, TIF2 has been shown to exhibit all the properties expected for a TIF/mediator of AF-2: it interacts directly with the LBDs of several NRs in an agonist- and AF-2-integrity-dependent manner *in vitro*

and *in vivo*, harbours an autonomous AF, relieves NR autosquelching, and enhances the activity of NR AF-2s when overexpressed in mammalian cells.

Thus, in one aspect, the present invention provides isolated nucleic acid molecules comprising a polynucleotide encoding TIF2 whose amino acid sequence is shown in Figure 1 (SEQ ID NO:2) or a fragment thereof. In another aspect, the invention provides isolated nucleic acid molecules encoding TIF2 having an amino acid sequence as encoded by the cDNA deposited as ATCC Deposit No. 97612.

The invention further provides an isolated nucleic acid molecule that hybridizes under stringent conditions to the above-described nucleic acid molecules. The present invention also relates to variants of the nucleic acid molecules of the present invention, which encode fragments, analogs or derivatives of the TIF2 protein, *e.g.*, polypeptides having at least one biological activity that is substantially similar to at least on biological activity of the TIF2 protein.

The present invention is further directed to isolated nucleic acid molecules that encode a cytoplasmic TIF2 polypeptide. Methods for generating nucleic acid molecules that encode a cytoplasmic TIF2 polypeptide include mutating or deleting the NLSs-coding N-terminal region of the nucleotide sequence shown in Figure 1 (SEQ ID NO:1). Preferably, nucleic acid molecules encoding a cytoplasmic TIF2 polypeptide will be fragments having a deletion in all or part of the N-terminal NLSs coding region. By the invention, the cytoplasmic TIF2 polypeptides described herein display at least one biological activity that is substantially similar to at least one biological activity of TIF2.

Further embodiments of the invention include isolated nucleic acid molecules comprising a polynucleotide having a nucleotide sequence at least 90% identical, and more preferably at least 95%, 96%, 97%, 98%, or 99% identical to the above described nucleic acid molecules.

The present invention also relates to vectors which contain the above-described isolated nucleic acid molecules, host cells transformed with the vectors and the production of TIF2 polypeptides by recombinant methods.

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The present invention further provides isolated TIF2 polypeptides having the amino acid sequence shown in Figure 1 (SEQ ID NO:2). In a further aspect, isolated TIF polypeptides are provided having an amino acid sequence as encoded by the cDNA deposited as ATCC Deposit No. 97612.

Screening methods are also provided for identifying agonists and antagonists of nuclear receptor AF-2 function, for identifying agonists and antagonists of TIF2 AD1 activity, and for identifying agonists and antagonists of TIF2 AD2 activity. Also provided are TIF2 antibodies.

Brief Description of the Figures

Figure 1(a-b). The nucleotide (SEQ ID NO:1) and amino acid (SEQ ID NO:2) sequences of the transcriptional intermediary factor-2 (TIF2) protein. This protein has a deduced molecular weight of about 160 kDa. The amino acid sequence of the functional coactivator TIF2.1 protein fragment is shown from amino acid residue 624 to residue 1287.

Figure 2(a-c). TIF2 is the 160-kDa nuclear-receptor-interacting factor.

(a) GST pull-down experiments identify a 160-kDa protein interacting with liganded estrogen receptor (ER) and retinoic acid receptor (RAR)-α ligand binding domains (LBDs) (ER(DEF) and RARα(DEF), respectively). Note that less material was run in lane 5 than in lanes 1-4.

(b) Immunodepletion followed by Far-Western detection demonstrates identity of TIF2 with the biochemically identified 160-kDa protein. Open triangle, TIF2; arrowhead, TIF1; circle, antibody crossreaction to GST-ER(DEF). The pα-TIF2-immunodetected species smaller that TIF2 (lanes 2 and 6) most probably is a degradation product of TIF2, as it is removed by immunodepletion with mα-TIF2 (lanes 4 and 8).

(c) Northern blotting reveals a ≈9-kb TIF2 transcript in various human tissues.

Methods. **(a)** *In vivo* ^{35}S-Met-labeled MCF7 whole cell extracts (Cavaillès, V. *et al.*, *Proc. Natl. Acad. Sci. USA 91*:10009-100013 (1994)) twice precleared with GST-loaded glutathione sepharose, were incubated (Le Douarin, B. *et al.*, *EMBO J. 14*:2020-2033 (1995)) with GST, GST-hER (DEF) or GST-hRARα(DEF), in presence or absence of 10^{-6} M E2 or T-RA. Bound proteins were recovered with SDS sample buffer and revealed by fluorography (Amplify, Amersham) of SDS-polyacrylamide gels.

(b) HeLa whole cell extracts (2 ml in 500 mM NaCl, 250 mM TrisHCl pH 7.5, 20% glycerol, 5 mM DTT), were precleared with protein-G sepharose (400 µl) and treated with protein-G sepharose (3 x 400 µl) loaded with mα-TIF2 (raised against a synthetic peptide encompassing amino acids E624-Q643 coupled to ovalbumin) or non-specific mouse IgG serum. After further clearing with protein-G sepharose (400 µl), the supernatant was incubated (Le Douarin, B. *et al.*, *EMBO J. 14*:2020-2033 (1995)) with GST-hER(DEF) in presence or absence of E2(10^{-6}M). Retained proteins were recovered with SDS sample buffer, separated by SDS-PAGE and electroblotted on nitrocellulose membranes. Far Western blotting was as described (Cavaillès, V. *et al.*, *Proc. Natl. Acad. Sci. USA 91*:10009-100013 (1994)). For immunoblotting rabbit polyclonal antiserum (pα-TIF2), raised against purified (Chen, Z-P. *et al.*, *J. Biol. Chem. 269*:25770-25776 (1994)) recombinant *E. coli*-expressed His-tagged TIF2.1, was used. pα-TIF2 and rabbit polyclonal pα-TIF1 were diluted 1:2000 for ECL-based Western blotting (Amersham). All constructs used in this study were verified by DNA sequencing.

(c) Human Northern blot (Clonetech, No 7760-1; Lot 5x332) was revealed with ^{32}P-labeled TIF2.1. To confirm proportionate loading, the membrane was rehybridized with ^{32}P-labeled β-actin cDNA (Clonetech).

Figure 3(a-b). Amino acid sequence of TIF2: homology with SRC-1 indicates the existence of a novel family of NR mediators.

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(a) Alignment and amino acid sequences of TIF-2 (SEQ ID NO:2) and the steroid receptor coactivator SRC-1 (SEQ ID NO:3) (Onate, S.A. *et al., Science 270:*1354-1357 (1995)). Two charged clusters rich in acidic and basic amino acid residues, three serine/threonine (S/T)-rich regions and one glutamine-rich region are highlighted. The N-terminal charged cluster contains putative bipartite nuclear localization signals (NLSs) (overlined). The regions encoding TIF2.1 (amino acids 624 to 1287; functional coactivator fragment) and dnSRC-1 (amino acids 865 to 1061; dominant negative fragment) are indicated. An asterisk identifies the TIF2 stop codon. Note that TIF2.1 and dnSRC-1 do not overlap, indicating that dnSRC-1 may possibly contain a NR-interacting region distinct from that of TIF2.1.

(b) Schematic comparison of TIF2 and SRC-1. Percent identities (similarities in parentheses) of homologous regions are indicated. The N-terminal charged cluster harbouring the putative NLS and the C-terminal S/T-rich region of TIF2 are not, or only weakly, conserved in SRC-1.

Methods. 340,000 clones of a human placenta cDNA λEXlox expression library were screened with a ^{32}P-labeled GST-hER(DEF) probe in presence of 10^{-6}M E2 using the Far-Western technique (Cavaillès, V. *et al., Proc. Natl. Acad. Sci. USA 91:*10009-100013 (1994)). The 1992-bp insert corresponding to the initial clone (TIF2.1) was used to rescreen the same library. Five highly overlapping cDNA inserts covered a region of 6 kb containing a 1,464-amino acid ORF. All inserts were sequenced on both strands. Transient expression of the assembled cDNA inserts encompassing the predicted ORF yielded a 160-kDa protein.

Figure 4(a-n). *In vivo* and *in vitro* interactions of TIF2 with nuclear receptors.

(a) Overexpressed TIF2 protein is mostly localized in discrete nuclear bodies and excluded from nucleoli. A superposed image of Hoechst DNA staining and TIF2 immunostaining is shown.

(b-i) Cytoplasmic TIF2.1 interacts in an agonist-dependent manner with nuclear receptors in mammalian cells. Light staining indicates TIF2.1-NO colocalization.

(k-n) TIF2.1 directly interacts *in vitro* in an agonist-dependent manner with nuclear receptors, and point mutations within the AF-2 activation domain (AD) core abolish this interaction. WT, wild-type. Ligand concentrations for *n*: 9C-RA, T-RA and T3, 10^{-6} M; E2, $5x10^{-8}$M; OHT, $5x10^{-6}$M. The smaller immunodetected polypeptide is a degradation product of TIF2.1. Note that the anti-TIF2 serum weakly crossreacts with GST-hER(DEF).

Methods. (a-i) Cos-1 cells were transiently transfected with TIF2.1 (10 μg) either (a) alone or (b-i) in addition with the indicated NR expression vectors (10 μg, except RARα, 1μg) in absence or presence of the cognate ligand (10^{-6}M, except R5020, 10^{-8} M). In d-f HE0 (Webster, N.J. *et al.*, *Cell 54*:199-207 (1988)) was used. Immunocytofluorescence assays were as described (Kastner, P. *et al.*, *EMBO J. 11*: 629-642 (1992)). Images were recorded by confocal laser microscopy.

(k-n) GST interaction assays with *E. coli*-expressed recombinant TIF2.1 (Fig. 2b) were performed as described (Le Douarin, B. *et al.*, *EMBO J. 14*:2020-2033 (1995)). Bound proteins were revealed by Western blotting with pα-TIF2 antiserum (dilution 1:30,000), equal loading of affinity matrices was verified by SDS-PAGE and Coomassie staining. 'Input' lanes contain one third of TIF2.1 input.

Figure 5 (a-e). TIF2 contains an autonomous AF, "antisquelches", and stimulates NO-AF2 activity in an agonist-, promoter- and cell-dependent manner.

(a) Increasing amounts of GAL-TIF2.1 fusion protein (lanes 2-4) activates transcription of a cognate reporter in transfected cells. Fold-induction is given below the CAT assays.

(b) TIF2.1 partially reverses transcriptional autointerference of ER. Normalized CAT expression (mean ± s.e. of 4 independent experiments) is shown. Open circles, +E2, +TIF2; squares, +E2, -TIF2; crosses, +OHT, +TIF2.

(c) TIF2 enhances transactivation mediated by some NR AF-2s, but not that mediated by other transcription factors. Mean TIF2 stimulations of 3 independent experiments are given (variation ≤ 13%). Ligands: lanes 3-4, E2; lanes 7-8, DHT (dihydrotestosterone); lanes 11-12, R5020; lanes 15-16, T-RA.

(d) TIF2 enhances PR-mediated transcriptional activation from both a minimal (GRE-TATA) and a complex (MMTV) promoter; this stimulation is significantly greater in Cos-1 than in HeLa cells.

(e) TIF2 greatly enhances agonist-induced activation by ER in Cos-1 and more weakly in HeLa cells. Note that the weak, seemingly ligand-independent, TIF2-induction of ER (compare lanes 1 with 2 and 7 with 8) is due to residual estradiol in the culture medium. In *d* and *e*, TIF2 inductions of ≥ 3 experiments are shown (variation ≤ 10%).

Methods. With the exception of GAL-TIF2.1, TIF2.1 and TIF2, the construction of reporter plasmids and expression vectors has been described (Meyer, M-E. *et al., Cell 57*:433-442 (1989); Bocquel, M-T. *et al., Nucl. acids Res. 17*:2581-2595 (1989); Tasset, D. *et al., Cell 62*:1177-1187 (1990); Gronemeyer, H. and Laudet, V., *Protein Profile 2*:1173-1308 (1995); Webster, N. J. *et al., Cell 54*:199-207 (1988); Strähle, U. *et al., EMBO J. 7*:3389-3395 (1988); Seipel, K. *et al., EMBO J. 11*:4961-4968 (1992); Nagpal, S. *et al., EMBO J. 12*:2349-2360 (1993); Chen, J-Y. *et al., EMBO J. 14*:1187-1197 (1995)). CAT assays were performed as described (Bocquel, M-T. *et al., Nucl. Acids Res. 17*:2581-2595 (1989)).

(a) HeLa cells were cotransfected with 1 μg $(17m)_5$-βG-CAT and 10 μg GAL(1-147) or 1,3 and 10 μg GAL(1-147)-TIF2.1, respectively.

(b) HeLa cells were cotransfected with 5 μg Vit-tk-CAT and the indicated amount of HEG0, with or without 5 μg TIF2.1 in the presence of 10^{-6}

M E2 or OHT. CAT activity is given relative to that induced by 100 ng HEG0 in presence of E2.

(c) HeLa cells were cotransfected with 1 μg 17m-tk-CAT and 1 μg of the indicated GAL-fusion vectors with or without the addition of 3 μg TIF2 expression vector in presence or absence of 10^{-6}M ligand.

(d) HeLa (lanes 1-12) or Cos-1 (lanes 13-18) cells were transfected with 5 μg GRE-TATA-CAT (lanes 1-6) or 1 μg MMTV-CAT (lanes 7-18) together with 1 μg hPR with or without 3 μg TIF 2 in presence or absence of 10^{-6} M of the indicated ligand.

(e) Cos-1 cells were cotransfected with 1 μg Vit-tk-CAT and 1 μg HEG0 with or without 3 μg TIF2 in presence or absence of 10^{-6} M of the indicated ligands.

Figure 6 (a-b). Schematic representation of reporter genes (A) and receptor expression vectors (B) (see the Materials and Methods section of Nagpal *et al., EMBO J 12(6):*2349-2360 (1993) for a detailed description of construction). Sequences of mCRBPII (SEQ ID NO:11) and mCRBPII(17m-ERE)/CAT (SEQ ID NO:11) are indicated. Minus and plus numbers are with respect to the RNA start site (+1). In (B), the various regions (A-F) of wild-type RARs and RXRs, as well as their truncation mutants, substitution mutants and chimeric receptor constructs are schematically represented (not to scale) (see Zelent *et al., Nature 339:*714-717 (1989); Leid *et al., Trends Biochem. Sci. 17:*427-433 (1992); Leid *et al., Cell 68:*377-395 (1992); Nagpal *et al., Cell 70:*1007-1019 (1992); and Allenby *et al., Proc. Natl. Acad. Sci. USA 90:*30-34 (1993)). Numbers indicate the amino acid positions in the wild-type receptor. The positions of the amino acid substitutions are indicated with an arrow.

Figure 7(a-e). Mapping of TIF2 domains.

(a) Schematic representation of functional domains identified in TIF2. The various TIF2 constructs are denoted; expressed residues are given in

parentheses. Bold lines indicate expressed sequences. Constructs that score positive or negative for NR interaction, transactivation or CBP binding are identified on the right by "+" and "−" signs respectively; nd, not determined.

(b) Mapping of the nuclear receptor-interacting domain of TIF2. Glutathione-S-transferase (GST) pull-down experiments were performed with ^{35}S-labeled *in-vitro*-translated TIF2 polypeptides and bacterially produced GST, GST-hERα(DEF) and GST-hRARα(DEF) in the presence or absence of 10^{-6} M of the cognate ligand (E2, estradiol for ER; RA, all-*trans-retinoic* acid for RAR).

(c) Analysis of the transcriptional activity of GAL-TIF2 fusion proteins. Cos-1 and HeLa cells were transfected with 3 µg of plasmids expressing different regions of TIF2 fused to the DNA-binding domain of the yeast transcription factor GAL4 together with 1 µg of the $(17m)_5$-G-CAT reporter plasmid. CAT assays were performed as described (Bocquel, M.T. *et al., Nucl. Acids Res. 17*:2581-2595 (1989)). Quantitative data on CAT reporter expression were obtained either by phosphoimager analysis (BAS2000, Fuji) of ^{14}C-labeled CAT reaction products separated by thin-layer chromatography, or using the CAT ELISA Kit (Boehringer Mannheim). In all cases, CAT activities were normalized to the β-galactosidase concentrations resulting from cotransfection of 1 µg of pCMVβGal (gift from T. Lerouge) as internal control. Fold inductions above the GAL4 DBD value are indicated. The mean and standard deviation of at least three experiments are shown. A representative Western blot, illustrating the expression levels of the GAL4-TIF2 fusion proteins, expressed from 10 µg of the corresponding expression vectors, is shown on the left. The blot was revealed with mouse monoclonal antibodies 2GV3 and 3GV2 specific for GAL4 DBD and 2GV4B7 specific for VP16 activation domain.

(d) Mapping of the CBP-interacting domain of TIF2. GST pull-down experiments were performed with ^{35}S-labeled *in-vitro*-translated TIF2 polypeptides and bacterially produced GST and GST-CBP (expressing CBP residues 1872 to 2165).

(e) Two hybrid analysis of the CBP-TIF2 interaction in mammalian cells *in vivo*. HeLa cells were transfected with 0.2 µg of the GAL4 or GAL4-CBP (expressing CBP residues 1872 to 2165) expression vectors together with 0.2 µg of the VP16 or VP16-TIF2 expression vectors in the presence of 1 µg of $(17m)_5$-TATA-CAT reporter plasmid. Fold induction relative to the GAL-CBP activity is indicated. The mean of three experiments is shown; in each case, values varied by less than ±20%.

Figure 8(a-e). Mapping of the TIF2 nuclear receptor interacting domain (NID).

(a) Alignment of the TIF2 NID (SEQ ID NO:2) with the corresponding regions of SRC-1 (SEQ ID NO:3) and P/CIP (SEQ ID NO:5) and description of NID mutations. The three conserved regions are displayed with the corresponding amino acid numbers of hTIF2 or full-length hSRC-1 (F-SRC-1); the leucines pertaining to the three NR box motifs (I, II, III) are boxed. The various deletion and leucine-to-alanine point mutation constructs are denoted.

(b) Alignment of the TIF2 (SEQ ID NO:2) NR boxes with NR boxes identified in several cofactors: TIF1α (SEQ ID NO:6), RIP140 (SEQ ID NO:7), and TRIP3 (SEQ ID NO:8). The conserved leucines are boxed.

(c-d) Interaction of TIF2 NID mutants with NRs *in vitro*. GST affinity chromatography experiments were carried out with ^{35}S-labelled *in-vitro*-translated GAL4 DBD fusions of TIF2 deletion mutants (c) or TIF2.1 point mutants (d) and bacterially expressed GST and GST fusions of the ER(DEF) and RAR(DEF) in the absence or presence of 10^{-6} M estradiol or all-*trans-retinoic* acid, respectively. For quantification of point mutant interactions, see below.

(e) Effect of TIF2 NID point mutations on stimulation of NR AF-2 activity. Cos-1 cells were cotransfected with 1 µg of the $(17m)_5$-TATA-CAT reporter, 0.2 µg of GAL-hERα(EF) or GAL-mRXRα(DE), and 2.5 µg of the TIF2.1 wildtype or mutated fragments, as indicated. The reporter gene activation relative to the TIF2.1 wildtype activity and in presence of 10^{-6} M estradiol (E2)

or all-*trans-retinoic* acid (RA), respectively, is indicated for each mutant (black bars); for comparison, *in vitro* binding of the respective mutants relative to TIF2.1 wildtype binding in presence of ligand is indicated by the white bars. Each bar represents the mean value obtained from at least three (interaction) or at least four (transactivation) experiments, respectively; standard deviations are indicated. Note that the absolute values for TIF2.1 wildtype activity varied by ±16% when cotransfected with GAL-hERα(EF) and by ±34% when cotransfected with GAL-mRXRα(DE). In the *in-vitro*-interaction assays, the affinity of the TIF2.1 wildtype standard varied by less than ±25%. Expression levels of TIF2 mutants in the cells were verified by Western blot (not shown) with mouse monoclonal antibody 3Ti3F1, which is directed against an epitope outside the mutated area.

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Figure 9(a-c). Mapping of the TIF2 activation function-1 (AF-1) and interaction of the AF-1 domain with CBP.

(a) Alignment of the TIF2 AF-1 with the corresponding region of SRC-1 (SEQ ID NO:3) and P/CIP (SEQ ID NO:9). Description of TIF2 AF-1 deletion mutants and their properties. The regions of TIF2 and hSRC-1 predicted to fold into α-helices are boxed (PHD program). GAL-TIF2 constructs that score positive or negative for transactivation of a GAL4 reporter are identified on the right by "+" and "−" signs, respectively; nd, not determined.

(b) Transcriptional activation of TIF2 AF-1 mutants. Cos-1 and HeLa cells were cotransfected with 3 μg of plasmids expressing different mutants of the TIF2 AF-1 fused to the DNA-binding domain of the yeast transcription factor GAL4 together with 1 μg of the $(17m)_5$-G-CAT reporter plasmid. Fold inductions above the activation seen with the GAL4 DBD alone are indicated. The values represent the mean of at least three experiments. Note that all GAL4-TIF2 fusion proteins were expressed to similar levels, as revealed by Western blot with antibodies directed against GAL4 DBD (data not shown).

(c) Interaction of TIF2 AF-1 mutants with CBP *in vitro*. GST pull-down experiments were performed with ^{35}S-labeled *in-vitro*-translated GAL-TIF2 fusion

proteins and bacterially produced GST and GST-CBP. Note, that the GAL4 DBD on its own does not interact with the GST-CBP affinity matrix.

Figure 10(a-c). Identification of TIF2 AF-1 mutants which are impaired in both transcriptional activation and interaction with CBP.

(a) Transcriptional activation by TIF2.13 and TIF2.13 mutants. Cos-1 and HeLa cells were cotransfected with 3 μg of plasmids expressing the TIF2.13 region and the indicated TIF2.13 mutants fused to the DNA-binding domain of the yeast transcription factor GAL4 together with 1 μg of the $(17m)_5$-G-CAT reporter plasmid. Fold inductions above the GAL4 DBD 1-fold value are indicated. The mean and standard deviation obtained from at least four experiments are shown. The expression levels of the GAL4-TIF2.13 fusion proteins were confirmed by western blotting (data not shown).

(b) Interaction of TIF2.13 wildtype and TIF2.13 mutants with CBP in mammalian cells revealed by two hybrid analysis. HeLa cells were transfected with 0.2 μg of GAL4 or GAL-CBP expression vectors together with 0.2 μg of VP16 or VP16-TIF2.13 expression vectors in the presence of 1 μg of $(17m)_5$-TATA-CAT reporter plasmid. Data are represented as fold induction of the activity seen with GAL-CBP alone. The mean and standard deviation obtained from ten experiments are shown. The expression levels were confirmed by Western blotting with antibodies directed against GAL4 DBD and VP16 AAD (data not shown).

(c) Interaction of TIF2.13 wildtype and TIF2.13 mutants with CBP *in vitro*. GST pull-down experiments were performed with ^{35}S-labeled *in-vitro*-translated VP16-TIF2.13 polypeptides and bacterially produced GST and GST-CBP. Note that the VP16 activation domain on its own does not interact with GST-CBP.

Figure 11. The TIF2.1 coactivator fragment efficiently stimulates the ligand-dependent AF-2 of ER, RAR and RXR in yeast. No stimulatory effect of

TIF2.1 on the isolated AF-1 of ER (HE15) is observable. Plasmids expressing different regions of hERα (white), hRARα (grey) and mRXRα (black) fused to the ER DBD (hERα(C)) were introduced into the yeast reporter strain PL3(α) together with TIF2.1 as indicated. White boxes represent sequences of transformants that were grown in the presence or absence of 10^{-6} M of the cognate ligand (estradiol for ER, all-*trans-retinoic* acid for RAR, 9-*cis*-retinoic acid for RXR). OMP decase activities determined on each cell-free extract are expressed in nmol/min/mg protein; the mean and standard deviation of at least four experiments are shown.

Figure 12(a-d). The isolated nuclear receptor-interacting domain (NID) of TIF2 acts dominant-negatively on the transcriptional activation by the ER, RXR and RAR LBDs. The mean value of induction obtained from the quantitation of at least three experiments (relative to the respective receptor LBD activity in absence of recombinant TIF2) is indicated below each panel. Expression levels of TIF2, TIF2.1 and TIF2.5 were routinely verified by Western blot with mouse monoclonal antibody 3Ti3C11 directed against a region of TIF2.5 (not shown).

(a) Overexpression of the TIF2.5 fragment containing the isolated NID reverses the stimulatory effect of the potent coactivator fragment TIF2.1. Cos-1 cells were cotransfected with 1 μg of the $(17m)_5$-TATA-CAT reporter and 0.2 μg GAL-ERα(EF) expression vector in the presence or absence of 10^{-6} M estradiol. Where indicated, 0.1 μg of TIF2.1 and 2.5 μg of TIF2.5 expression vectors were cotransfected in addition.

(b-d) Full length TIF2 and the coactivator fragment TIF2.1 enhance, whereas the nuclear receptor interacting domain TIF2.5 blocks the activity of the ER, RXR and RAR LBDs. Cos-1 and HeLa cells were cotransfected with 1 μg of the $(17m)_5$-TATA-CAT reporter and 0.2 μg of the expression vector encoding the respective GAL DBD-fusion of hERα(EF), mRXRα(DE) or mRARα(DEF). In the presence or absence of 10^{-6} M ligand (E2, estradiol; 9C-RA, 9-*cis*-retinoic

acid; T-RA, all-*trans-retinoic* acid), together with 0.25 μg or 2.5 μg of TIF2, TIF2.1 and TIF2.5 expression vectors.

Detailed Description of the Preferred Embodiments

The present invention provides isolated nucleic acid molecules comprising a polynucleotide encoding transcriptional intermediary factor-2 (TIF2) whose amino acid sequence is shown in Figure 1 (SEQ ID NO:2). The TIF2 protein of the present invention shares sequence homology with the human steroid receptor coactivator SRC-1 (SEQ ID NO:3) (Figure 3). The nucleotide sequence shown in Figure 1 (SEQ ID NO:1) was obtained by sequencing a cDNA clone which was deposited on June 14, 1996 at the ATCC and given accession number 97612.

Nucleic Acid Molecules

In one embodiment of the present invention, isolated nucleic acid molecules are provided which encode the TIF2 protein. Sequence similarities between TIF2 and SRC-1 (Onate *et al., Science 270:*1354 (1995)) indicate the existence of a novel gene family of NR transcriptional mediators. Using information provided herein, such as the nucleotide sequence in Figure 1 (SEQ ID NO:1) or the above-described deposited clone, a nucleic acid molecule of the present invention encoding a TIF2 polypeptide may be obtained using standard cloning and screening procedures. Illustrative of the invention, the nucleic acid molecule described in Figure 1 (SEQ ID NO:1) was discovered in a cDNA expression library from human placenta tissue. The TIF2 cDNA of the present invention encodes a protein of about 159 kDa (1,464 amino acids), which includes N-terminal nuclear localization signals (NLSs), one Gln- and three Ser/Thr-rich regions, and two charged clusters (Figure 3). TIF2 is widely expressed, since the corresponding transcript was found in several human tissues, including pancreas, kidney, muscle, liver, lung, placenta, brain and heart (Figure 2c).

Isolated nucleic acids of the present invention may be in the form of RNA, such as mRNA, or in the form of DNA, including, for instance, cDNA and genomic DNA obtained by cloning or produced synthetically. The DNA may be double-stranded or single-stranded. Single-stranded DNA or RNA may be the coding strand, also known as the sense strand, or it may be the non-coding strand, also referred to as the anti-sense strand.

By "isolated" nucleic acid molecule(s) is intended a nucleic acid molecule, DNA or RNA, which has been removed from its native environment. For example, recombinant DNA molecules contained in a vector are considered isolated for purposes of the present invention. Additional illustrative examples of isolated DNA molecules include recombinant DNA molecules maintained in heterologous host cells and purified (partially or substantially) DNA molecules in solution. Isolated RNA molecules include *in vitro* RNA transcripts of the DNA molecules of the present invention as well as partially or substantially purified mRNA molecules. Isolated nucleic acid molecules according to the present invention further include such molecules produced synthetically.

Isolated nucleic acid molecules of the present invention include DNA molecules comprising an open reading frame (ORF) with an initiation codon at position 163-165 of the nucleotide sequence shown in Figure 1 (SEQ ID NO:1); and DNA molecules which comprise a sequence substantially different than that described above but which, due to the degeneracy of the genetic code, still encode the TIF2 protein. Of course, the genetic code is well known in the art. Thus, it would be routine for one skilled in the art to generate the degenerate variants described above.

In another aspect, the invention provides isolated nucleic acid molecules encoding the TIF2 polypeptide having an amino acid sequence as encoded by the cDNA clone deposited as ATCC Deposit No. 97612 on June 14, 1996 (American Type Culture Collection, (ATCC) Rockville, MD). The invention further provides an isolated nucleic acid molecule having the nucleotide sequence shown in Figure 1 (SEQ ID NO:1) or the nucleotide sequence of the TIF2 cDNA contained in the

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above-described clone, or a nucleic acid molecule having a sequence complementary to one of the above sequences. Such isolated nucleic acid molecules, preferably DNA molecules, are useful as probes for gene mapping by *in situ* hybridization with chromosomes and for detecting expression of the TIF2 gene in human tissue, for instance, by Northern blot analysis.

In another aspect, the invention provides an isolated nucleic acid molecule that hybridizes under stringent conditions to the above-described nucleic acid molecules. As used herein "stringent conditions" is intended to mean, as a non-limiting example, overnight incubation at 42°C in a solution comprising 50% formamide, 5xSSC (150 mM NaCl, 15mM trisodium citrate), 50 mM sodium phosphate (pH7.6), 5x Denhardt's solution, 10% dextran sulfate, and 20 µg/ml denatured, sheared salmon sperm DNA, followed by washing the filters in 0.1xSSC at about 65°C. Preferably, such "an isolated nucleic acid molecule that hybridizes under stringent conditions" will be at least 15 bp, preferably at least 20 bp, more preferably at least 30 bp, and most preferably, at least 50 bp in length.

As used herein, "fragments" of an isolated DNA molecule having the nucleotide sequence of the deposited cDNA or the nucleotide sequence as shown in Figure 1 (SEQ ID NO:1) is intended to mean DNA fragments at least 15 bp, more preferably at least 20 bp, and most more preferably at least 30 bp in length which are useful as diagnostic probes and primers as discussed above and in more detail below. Larger DNA fragments, up to, for example, 500 bp in length, are also useful as probes according to the present invention. A fragment of at least 20 bp in length, for example, is intended to mean fragments which include 20 or more contiguous bases from the nucleotide sequence of the deposited cDNA or the nucleotide sequence as shown in Figure 1 (SEQ ID NO:1). As indicated, such fragments are useful diagnostically either as a probe according to conventional DNA hybridization techniques or as primers for amplification of a target sequence by the polymerase chain reaction (PCR).

Since the gene has been deposited and the nucleotide sequence shown in Figure 1 (SEQ ID NO:1) is provided, generating such DNA fragments would be

routine to the skilled worker in the relevant art. Restriction endonuclease cleavage or shearing by sonication, for example, may easily be used to generate fragments of various sizes. Alternatively, the DNA fragments of the present invention can be generated synthetically according to the methods and techniques known and available to those skilled in the art. Ten expressed sequence tags with homology to part of the TIF-2 nucleoide sequence were identified by the inventors in GenBank: GenBank Accession numbers T77249, R77864, T77464, R77770, R08880, T85560, R25318, T85561, R08986 and R26517.

The present invention further relates to variants of the nucleic acid molecules of the present invention, which encode for fragments, analogs or derivatives of the TIF2 protein, *e.g.*, polypeptides having biological activity substantially similar to the TIF2 protein. Variants may occur naturally, such as isoforms and allelic variants. Non-naturally occurring variants may be produced using any of the mutagenesis techniques known and available to those skilled in the art.

Such variants include those produced by nucleotide substitutions, deletions or additions. The substitutions, deletions or additions may involve one or more nucleotides. The variants may be altered in coding or non-coding regions or both. Alterations in the coding regions may produce conservative or non-conservative amino acid substitutions, deletions or additions. Especially preferred among these are silent substitutions, additions and deletions, which do not alter the properties and activities of the TIF2 protein or fragment thereof. Also especially preferred in this regard are conservative substitutions.

The present invention is further directed to isolated nucleic acid molecules that encode a cytoplasmic TIF2 polypeptide. Full-length TIF2 is a nuclear protein due to the presence of N-terminal nuclear localization signals (NLSs) (Figure 3). By a "cytoplasmic TIF2 polypeptide", is intended a TIF2 polypeptide that is essentially found in the cytoplasm after being recombinantly expressed in mammalian cells. Methods for generating nucleic acid molecules that encode a cytoplasmic TIF2 polypeptide include mutating or deleting the NLSs-coding

N-terminal region of the nucleotide sequence shown in Figure 1 (SEQ ID NO:1). Examples of NLS sequences include amino acids 13-20 and 31-39 and nucleotides 199-222 and 253-279 of Figure 1 (*See also,* Figure 3). Suitable mutations to the NLSs-coding N-terminal region include substitutions, deletions and insertions which result in a nucleic acid molecule that encodes a TIF2 polypeptide lacking the nuclear localization function. Methods for generating such mutations will be readily apparent to the skilled artisan and are described, for instance, in *Molecular Cloning, A Laboratory Manual,* 2nd edition, edited by Sambrook, J., Fritsch, E.F. and Maniatis, T., (1989), Cold Spring Harbor Laboratory Press.

Preferably, nucleic acid molecules encoding a cytoplasmic TIF2 polypeptide will be fragments having a deletion in all or part of the N-terminal NLSs coding region. Methods for generating such fragments are described below. According to the present invention, such nucleic acid fragments further include N-terminal deletions extending beyond the NLSs coding region and may also include C-terminal deletions. For example, the present inventors have generated a nucleic acid molecule encoding the cytoplasmic TIF2.1 polypeptide (amino acids 624 to 1287 in Figures 1 and 3 (SEQ ID NO: 2)), which, like the nuclear full-length TIF2, interacts in an agonist-dependent manner with the nuclear receptors and enhances nuclear receptor-mediated transcriptional activation. The present inventors have also generated a nucleic acid molecule encoding the cytoplasmic TIF2.5 polypeptide (amino acids 624-869 in Figures 1 and 3 (SEQ ID NO:2)), which interacts with the NID domain of nuclear receptors, but does not enhance transcription. Also generated were nucleic acids encoding the cytoplasmic TIF2.8 and TIF 2.12 polypeptides (amino acids 1010-1179 and amino acids 940-1131, respectively, in Figures 1 and 3 (SEQ ID NO:2), which enhance transcription, but do not bind to nuclear receptors. Thus, by the invention, nucleic acid molecules are provided encoding cytoplasmic TIF2 polypeptides that interact in an agonist-dependent manner with nuclear receptors and enhance nuclear receptor-mediated transcriptional activation. Also provided are cytoplasmic TIF2 polypeptides that bind to nuclear receptors, but do not enhance transcription as

are provided cytoplasmic TIF2 polypeptides that enhance transcription, but do not bind to nuclear receptors. As the skilled artisan will recognize, the length of such nucleic acid molecules can vary.

Further embodiments of the invention include isolated nucleic acid molecules comprising a polynucleotide having a nucleotide sequence at least 90% identical, and more preferably at least 95%, 96%, 97%, 98%, or 99% identical to: (a) the nucleotide sequence of the cDNA deposited as ATCC 97612; (b) the nucleotide sequence shown in Figure 1 (SEQ ID NO:1); (c) the nucleotide sequence of the cDNA deposited as ATCC 97612 which encodes the full-length TIF2 protein; (d) the nucleotide sequence shown in Figure 1 (SEQ ID NO:1), which encodes the full-length TIF2 protein; (e) the nucleotide sequence of the cDNA deposited as ATCC 97612, which encodes the functional coactivator TIF2.1 protein; (f) the nucleotide sequence shown in Figure 1 (SEQ ID NO:1), which encodes the functional coactivator TIF2.1 protein; (g) the nucleotide sequence shown in Figure 1 (SEQ ID NO:1) which encodes the TIF2.0 polypeptide; (h) the nucleotide sequence shown in Figure 1 (SEQ ID NO:1) which encodes the TIF2.2 polypeptide; (i) the nucleotide sequence shown in Figure 1 (SEQ ID NO:1) which encodes the TIF2.3 polypeptide; (j) the nucleotide sequence shown in Figure 1 (SEQ ID NO:1) which encodes the TIF2.4 polypeptide; (k) the nucleotide sequence shown in Figure 1 (SEQ ID NO:1) which encodes the TIF2.5 polypeptide; (l) the nucleotide sequence shown in Figure 1 (SEQ ID NO:1) which encodes the TIF2.6 polypeptide; (m) the nucleotide sequence shown in Figure 1 (SEQ ID NO:1) which encodes the TIF2.7 polypeptide; (n) the nucleotide sequence shown in Figure 1 (SEQ ID NO:1) which encodes the TIF2.8 polypeptide; (o) the nucleotide sequence shown in Figure 1 (SEQ ID NO:1) which encodes the TIF2.9 polypeptide; (p) the nucleotide sequence shown in Figure 1 (SEQ ID NO:1) which encodes the TIF2.10 polypeptide; (q) the nucleotide sequence shown in Figure 1 (SEQ ID NO:1) which encodes the TIF2.12 polypeptide; and (r) a nucleotide sequence complementary to any of the nucleotide sequences in (a-q).

Whether any two nucleic acid molecules have nucleotide sequences that are at least 90%, 95%, 96%, 97%, 98%, or 99% "identical" can be determined conventionally using known computer algorithms such as the "fastA" program using, for example, the default parameters (Pearson and Lipman, *Proc. Natl. Acad. Sci. USA 85:*2444 (1988)). The present application is directed to such nucleic acid molecules having a nucleotide sequence at least 90%, 95%, 96%, 97%, 98%, 99%, identical to the nucleotide sequence of the above-recited nucleic acid molecules irrespective of whether they encode a polypeptide having TIF2 activity. This is because, even where a particular nucleic acid molecule does not encode a polypeptide having TIF2 activity, one of skill in the art would still know how to use the nucleic acid molecule as a probe. Uses of the nucleic acid molecules of the present invention that do not encode a polypeptide having TIF2 activity include, *inter alia,* (1) isolating the TIF2 gene or allelic variants thereof in a cDNA library; (2) *in situ* hybridization (FISH) to metaphase chromosomal spreads to provide precise chromosomal location of the TIF2 gene as described in Verma *et al., Human Chromosomes: a Manual of Basic Techniques*, Pergamon Press, New York (1988); and Northern Blot analysis for detecting TIF2 mRNA expression in specific tissues, such as placenta tissue.

Preferred, however, are nucleic acid molecules having a nucleotide sequence at least 90%, and preferably at least 95%, 96%, 97%, 98%, or 99% identical to the nucleotide sequence of the above-described nucleic acid molecules which do, in fact, encode a polypeptide having at least one TIF2 protein activity. As used herein, "a polypeptide having a TIF2 protein activity" is intended to mean polypeptides exhibiting similar, but not necessarily identical, activity as at least one biological activity of the TIF2 protein as measured in a particular biological assay. For example, the TIF2 protein of the present invention interacts directly in an agonist-dependent manner with the ligand binding domains of several nuclear receptors. Moreover, when recombinantly expressed in mammalian cells, the TIF2 protein of the present invention enhances transcription via CBP-dependent and CBP-independent routes.

Thus, "a polypeptide having a TIF2 protein activity" includes polypeptides having one or more of the following activities: interaction with the LBD of one or more NRs in an agonist-dependent manner; enhancement of CBP-dependent transcriptional activation; or enhancement of CBP-independent transcriptional activation.

Screening assays for determining whether a candidate polypeptide has TIF2 protein activity are described in detail in Examples 1, 3, 4, and 6 below. For example, by performing such assays, the present inventors have discovered that the functional coactivator fragment TIF2.1 (amino acids 624 to 1287 in Figures 1 and 3 (SEQ ID NO: 2)) is "a polypeptide having a TIF2 protein activity." The present inventors have also discovered that the fragment TIF2.5 (amino acids 624-869) binds to the LBD of NRs without activating transcription, and is "a polypeptide having a TIF2 protein activity." Also discovered was the fragment TIF2.2 (amino acids 1288-1464 as shown in Figure 1 (SEQ ID NO:2)), which enhances CBP-independent transcription. Thus, TIF2.2 is "a polypeptide having a TIF2 protein activity." Another fragment discovered by the inventors, TIF 2.8 (amino acids 1010-1179 as shown in Figure 1 (SEQ ID NO:2)) is a "polypeptide having a TIF2 protein activity" as it activates CBP-dependent transcription.

Due to the degeneracy of the genetic code, one of ordinary skill in the art will immediately recognize that a large number of the nucleic acid molecules having a nucleotide sequence at least 90%, preferably at least 95%, 96%, 97%, 98%, 99% identical to the nucleotide sequence of the above-described nucleic acid molecules will encode "a polypeptide having a TIF2 protein activity." In fact, since degenerate variants all encode the same polypeptide, this will be clear to the skilled artisan even without performing the above described screening assays. It will be further recognized by those skilled in the art that, for such nucleic acid molecules that are not degenerate variants, a reasonable number will also encode a polypeptide having a TIF2 protein activity. This is because the skilled artisan is fully aware of possible amino acid substitutions that are either less likely or not

likely to significantly affect protein function (*e.g.*, replacing one aliphatic amino acid with a second aliphatic amino acid).

Guidance concerning how to make phenotypically silent amino acid substitutions is provided, for example, in J.U. Bowie *et al.*, "Deciphering the Message in Protein Sequences: Tolerance to Amino Acid Substitutions," *Science 247:*1306-1310 (1990), wherein the authors indicate that there are two main approaches for studying the tolerance of an amino acid sequence to change. The first method relies on the process of evolution, in which mutations are either accepted or rejected by natural selection. The second approach uses genetic engineering to introduce amino acid changes at specific positions of a cloned gene and selections or screens to identify sequences that maintain functionality. As the authors state, these studies have revealed that proteins are surprisingly tolerant of amino acid substitutions. The authors further indicate which amino acid changes are likely to be permissive at a certain position of the protein. For example, most buried amino acid residues require nonpolar side chains, whereas few features of surface side chains are generally conserved. Other such phenotypically silent substitutions are described in Bowie *et al., supra,* and the references cited therein.

Vectors and Host Cells

The present invention also relates to vectors which include the isolated DNA molecules of the present invention, host cells which are genetically engineered with the recombinant vectors, and the production of TIF2 polypeptides or fragments thereof, such as TIF2.1, by recombinant techniques.

Recombinant constructs may be introduced into host cells using well known techniques such infection, transduction, transfection, transvection, electroporation and transformation. The vector may be, for example, a phage, plasmid, viral or retroviral vector. Retroviral vectors may be replication competent or replication defective. In the latter case, viral propagation generally will occur only in complementing host cells.

The polynucleotides may be joined to a vector containing a selectable marker for propagation in a host. Generally, a plasmid vector is introduced in a precipitate, such as a calcium phosphate precipitate, or in a complex with a charged lipid. If the vector is a virus, it may be packaged *in vitro* using an appropriate packaging cell line and then transduced into host cells.

Preferred are vectors comprising cis-acting control regions to the polynucleotide of interest. Appropriate trans-acting factors may be supplied by the host, supplied by a complementing vector or supplied by the vector itself upon introduction into the host.

In certain preferred embodiments in this regard, the vectors provide for specific expression, which may be inducible and/or cell type-specific. Particularly preferred among such vectors are those inducible by environmental factors that are easy to manipulate, such as temperature and nutrient additives.

Expression vectors useful in the present invention include chromosomal-, episomal- and virus-derived vectors, e.g., vectors derived from bacterial plasmids, bacteriophage, yeast episomes, yeast chromosomal elements, viruses such as baculoviruses, papova viruses, vaccinia viruses, adenoviruses, fowl pox viruses, pseudorabies viruses and retroviruses, and vectors derived from combinations thereof, such as cosmids and phagemids.

The DNA insert should be operatively linked to an appropriate promoter, such as the phage lambda PL promoter, the E. coli lac, trp and tac promoters, the SV40 early and late promoters and promoters of retroviral LTRs, to name a few. Other suitable promoters will be known to the skilled artisan. The expression constructs will further contain sites for transcription initiation, termination and, in the transcribed region, a ribosome binding site for translation. The coding portion of the mature transcripts expressed by the constructs will preferably include a translation initiating AUG at the beginning and a termination codon (UAA, UGA or UAG) appropriately positioned at the end of the polypeptide to be translated.

As indicated, the expression vectors will preferably include at least one selectable marker. Such markers include dihydrofolate reductase or neomycin

resistance for eukaryotic cell culture and tetracycline or ampicillin resistance genes for culturing in E. coli and other bacteria. Representative examples of appropriate hosts include, but are not limited to, bacterial cells, such as E. coli, Streptomyces and Salmonella typhimurium cells; fungal cells, such as yeast cells; insect cells such as Drosophila S2 and Spodoptera Sf9 cells; animal cells such as CHO, Cos and Bowes melanoma cells; and plant cells. Appropriate culture mediums and conditions for the above-described host cells are known in the art.

Illustrative examples of vectors preferred for use in bacteria include, but are not limited to, pA2, pQE70, pQE60 and pQE-9, available from Qiagen; pBS vectors, Phagescript vectors, Bluescript vectors, pNH8A, pNH16a, pNH18A, pNH46A, available from Stratagene; and ptrc99a, pKK223-3, pKK233-3, pDR540, pRIT5 available from Pharmacia. Preferred eukaryotic vectors include, but are not limited to, pWLNEO, pSV2CAT, pOG44, pXT1 and pSG available from Stratagene; and pSVK3, pBPV, pMSG and pSVL available from Pharmacia. Other suitable vectors will be readily apparent to the skilled artisan.

Among known bacterial promoters suitable for use in the present invention include the E. coli lacI and lacZ promoters, the T3 and T7 promoters, the gpt promoter, the lambda PR and PL promoters and the trp promoter. Suitable eukaryotic promoters include the CMV immediate early promoter, the HSV thymidine kinase promoter, the early and late SV40 promoters, the promoters of retroviral LTRs, such as those of the Rous sarcoma virus ("RSV"), and metallothionein promoters, such as the mouse metallothionein-I promoter.

Introduction of the construct into the host cell can be effected by calcium phosphate transfection, DEAE-dextran mediated transfection, cationic lipid-mediated transfection, electroporation, transduction, infection or other methods. Such methods are described in many standard laboratory manuals, such as Davis *et al.*, *Basic Methods in Molecular Biology* (1986).

Transcription of the DNA encoding the polypeptides of the present invention by higher eukaryotes may be increased by inserting an enhancer sequence into the vector. Enhancers are cis-acting elements of DNA, generally

about 10 to 300 bp in size, that act to increase transcriptional activity of a promoter in a given host cell-type. Illustrative examples of enhancers include, but are not limited to, the SV40 enhancer, which is located on the late side of the replication origin at bp 100 to 270, the cytomegalovirus early promoter enhancer, the polyoma enhancer on the late side of the replication origin, and adenovirus enhancers.

For secretion of the translated protein into the lumen of the endoplasmic reticulum, into the periplasmic space or into the extracellular environment, appropriate secretion signals may be incorporated into the expressed polypeptide. The signals may be endogenous to the polypeptide or they may be heterologous signals.

The polypeptide may be expressed in a modified form, such as a fusion protein, and may include not only secretion signals, but also additional heterologous functional regions. Thus, for instance, a region of additional amino acids, particularly charged amino acids, may be added to the N-terminus of the polypeptide to improve stability and persistence in the host cell, during purification, or during subsequent handling and storage. Also, peptide moieties may be added to the polypeptide to facilitate purification.

The TIF2 protein or fraction thereof can be recovered and purified from recombinant cell cultures by well-known methods including ammonium sulfate or ethanol precipitation, acid extraction, anion or cation exchange chromatography, phosphocellulose chromatography, hydrophobic interaction chromatography, affinity chromatography, hydroxylapatite chromatography and lectin chromatography. Most preferably, high performance liquid chromatography ("HPLC") is employed for purification.

Polypeptides of the present invention include, but are not limited to, naturally purified products, products of chemical synthetic procedures, and products produced by recombinant techniques from a prokaryotic or eukaryotic host, including, for example, bacterial, yeast, higher plant, insect and mammalian cells. Depending upon the host employed in a recombinant production procedure,

the polypeptides of the present invention may be post translationally modified (e.g., glycosylated, phosphorylated, farnesylated, etc.). In addition, polypeptides of the invention may also include an initial modified methionine residue, in some cases as a result of host-mediated processes.

TIF2 Polypeptides and Fragments

The invention further provides an isolated TIF2 polypeptide having the amino acid sequence encoded by the deposited cDNA, or the amino acid sequence as shown in Figure 1 (SEQ ID NO:2), or a fragment thereof. Preferred polypeptide fragments will have a TIF2 protein activity. In order for a TIF2 polypeptide to interact in an agonist-dependent manner with nuclear receptors and to enhance nuclear receptor-mediated transcriptional activation, such TIF2 polypeptide fragments should at least include amino acid residues 624 to 1131 as shown in Figure 1(SEQ ID NO:2) or amino acid substitutions, additions or deletions thereof that are not significantly detrimental to the polypeptides' ability to interact in an agonist-dependent manner with nuclear receptors and to enhance nuclear receptor-mediated transcriptional activation. In order for a TIF2 polypeptide fragment to interact with the LBD of an NR without activating transcription, the TIF2 polypeptide fragments should at least include amino acids 624-869 as shown in Figure 1 (SEQ ID NO:2), or amino acid substitutions, additions or deletions thereof that are not significantly detrimental to the polypeptides' ability to interact with the LBD of an NR. In order for a TIF2 polypeptide fragment to activate CBP-dependent transcription, the TIF2 polypeptide should at least include amino acid residues 1010-1131 as shown in Figure 1 (SEQ ID NO:2) or amino acid substitutions, additions or deletions thereof that are not significantly detrimental to the polypeptides' ability to activate CBP-dependent transcription. For a TIF2 polypeptide to activate CBP-independent transcription, the TIF2 polypeptide should at least include amino acid residues 1288-1464 as shown in Figure 1 (SEQ ID NO:2) or amino acid

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substitutions, additions or deletions thereof that are not significantly detrimental to the polypeptides' ability to activate CBP-indepentent transcription.

Exemplary TIF2 polypeptide fragments according to the present invention include cytoplasmic TIF2 polypeptides having at least one mutation or deletion in a N-terminal NLS region that interferes with the nuclear localization function. Methods for generating cytoplasmic TIF2 polypeptides are described above.

As used herein, an "isolated" polypeptide or protein is intended to mean a polypeptide or protein removed from its native environment, such as recombinantly produced polypeptides and proteins expressed in host cells and native or recombinant polypeptides which have been substantially purified by any suitable technique (*e.g.*, the single-step purification method disclosed in Smith and Johnson, *Gene 67:*31-40 (1988), which is incorporated by reference herein). Isolated polypeptides or proteins according to the present invention further include such compounds produced synthetically.

The present inventors have discovered that the full-length TIF2 protein is an about 1464 amino acid residue protein with a deduced molecular weight of about 160 kDa. It will be recognized by those skilled in the art that some amino acid sequence of the TIF2 protein can be varied without significant effect on the structure or function of the protein. If such differences in sequence are contemplated, it should be remembered that there will be critical areas on the protein which determine activity, such as the region described above which has been determined by the inventors as being critical to the protein's ability to enhance nuclear receptor-mediated transcriptional activation. In general, it is often possible to replace residues which form the tertiary structure, provided that residues performing a similar function are used. In other instances, the type of residue may be completely unimportant if the alteration occurs at a non-critical region of the protein.

Thus, the present invention further includes variations of the TIF2 polypeptide which show substantial TIF2 polypeptide activity or which include regions of TIF2 protein such as the protein fragments discussed below. Such

mutants include deletions, insertions, inversions, repeats, and type substitutions (for example, substituting one hydrophilic residue for another, but not strongly hydrophilic for strongly hydrophobic as a rule). Small changes or such "neutral" amino acid substitutions will generally have little effect on activity.

Typically seen as conservative substitutions are the replacements, one for another, among the aliphatic amino acids Ala, Val, Leu and Ile; interchange of the hydroxyl residues Ser and Thr, exchange of the acidic residues Asp and Glu, substitution between the amide residues Asn and Gln, exchange of the basic residues Lys and Arg and replacements among the aromatic residues Phe and Tyr.

As indicated in detail above, further guidance concerning which amino acid changes are likely to be phenotypically silent (*i.e.*, not likely to have a significant deleterious effect on a function) can be found in Bowie *et al.*, "Deciphering the Message in Protein Sequences: Tolerance to Amino Acid Substitutions," *Science 247:*1306-1310 (1990)).

The polypeptides of the present invention include polypeptides having an amino acid sequence as encoded by the deposited cDNA, an amino acid sequence as shown in SEQ ID NO:2, as well as an amino acid sequence at least 80% identical, more preferably at least 90% identical, and most preferably at least 95%, 96%, 97%, 98%, or 99% identical, to the amino acid sequence encoded by the deposited cDNA, to the amino acid sequence as shown in SEQ ID NO:2, or to the amino acid sequence of a polypeptide fragment described above. Whether two polypeptides have an amino acid sequence that is at least 80%, 90% or 95% identical can be determined using a computer algorithm as described above.

As described in detail below, the nucleic acid molecules and polypeptides of the present invention are useful in screening assays for identifying agonist and antagonist of NR AF2-mediated transactivation. For example, in Halachmi, S., *et al., Science 264*: 1455 (1994), the authors show that tamoxifen, which has growth inhibitory effects in breast cancer, disrupts the formation of a complex that includes the estrogen receptor and ERAP160. Accordingly, the nucleic acid molecules and polypeptides of the present invention are useful in assays for

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identifying drugs capable of enhancing or inhibiting nuclear receptor-mediated pathways.

The nucleic acid molecules and polypeptides of the present invention are useful in screening assays for identifying agonists and antagonists of TIF2 AD1 activity, and in screening assays for identifying agonist and antagonists of TIF2 AD2 activity, as described in detail below.

Screening Methods

Nuclear receptors (NRs) are members of a superfamily of ligand-inducible transcriptional regulatory factors that include steroid hormone, thyroid hormone, vitamin D3 and retinoid receptors (Leid, M., *et al., Trends Biochem. Sci. 17:*427-433 (1992); Leid, M., *et al., Cell 68:*377-395 (1992); and Linney, E. *Curr. Top. Dev. Biol., 27:*309-350 (1992)). NRs exhibit a modular structure which reflects the existence of several autonomous functional domains. Based on amino acid sequence similarity between the chicken estrogen receptor, the human estrogen and glucocorticoid receptors, and the v-erb-A oncogene, Krust, A., *et al., EMBO J. 5:*891-897 (1986), defined six regions, A, B, C, D, E and F (see Figure 6) , which display different degrees of evolutionary conservation amongst various members of the nuclear receptor superfamily. The highly conserved region C contains two zinc fingers and corresponds to the core of the DNA-binding domain (DBD), which is responsible for specific recognition of the cognate response elements. Region E is functionally complex, since in addition to the ligand-binding domain (LBD), it contains a ligand-dependent activation function (AF-2) and a dimerization interface. An autonomous transcriptional activation function (AF-1) is present in the non-conserved N-terminal A/B regions of the steroid receptors. Interestingly, both AF-1 and AF-2 of steroid receptors exhibit differential transcriptional activation properties which appear to be both cell type and promoter context specific (Gronemeyer, H. *Annu. Rev. Genet. 25:*89-123 (1991)).

The all-*trans* (T-RA) and 9-*cis* (9C-RA) retinoic acid signals are transduced by two families of nuclear receptors, RAR α, β and γ (and their isoforms) are activated by both T-RA and 9C-RA, whereas RXR α, β and γ are exclusively activated by 9C-RA (Allenby, G. *et al., Proc. Natl. Acad. Sci. USA 90:*30-34 (1993)). The three RAR types differ in their B regions, and their main isoforms (α1 and α2, β1-4, and γ1 and γ2) have different N-terminal A regions (Leid, M. *et al., Trends Biochem. Sci. 17:*427-433 (1992)). Similarly, the RXR types differ in their A/B regions (Mangelsdorf, D.J. *et al, Genes Dev. 6:*329-344 (1992)).

The E-region of RARs and RXRs has also been shown to contain a dimerization interface (Yu, V.C. *et al., Curr. Opin. Biotechnol. 3:*597-602 (1992)). Most interestingly, it was demonstrated that RAR/RXR heterodimers bind much more efficiently *in vitro* than homodimers of either receptor to a number of RA response elements (RAREs) (Yu, V.C. *et al., Cell 67*:1251-1266 (1991); Berrodin, T. J. *et al., Mol. Endocrinol 6*:1468-1478 (1992); Bugge, T. H. *et al., EMBO J. 11*:1409-1418 (1992); Hall, R. K. *et al., Mol. Cell. Biol. 12*: 5527-5535 (1992); Hallenbeck, P. L. *et al., Proc. Natl. Acad. Sci. USA 89*:5572-5576 (1992); Husmann, M. *et al., Biochem. Biophys. Res. Commun. 187*:1558-1564 (1992); Kliewer, S.A. *et al., Nature 355*:446-449 (1992b); Leid, M. *et al., Cell 68*:377-395 (1992); Marks, M. S. *et al., EMBO J. 11*:1419-1435 (1992); Zhang, X. K. *et al., Nature 355*:441-446 (1992)). RAR and RXR heterodimers are also preferentially formed in solution *in vitro* (Yu, V.C. *et al., Cell 67*:1251-1266 (1991); Leid, M. *et al., Cell 68*:377-395 (1992); Marks, M. S. *et al., EMBO J. 11*:1419-1435 (1992)), although the addition of 9C-RA appears to enhance the formation of RXR homodimers *in vitro* (Lehman, J. M. *et al., Science 258*:1944-1946 (1992); Zhang, X. K. *et al., Nature 358*:587-591 (1992b)). That RAR-RXR heterodimers, rather than the corresponding homodimers, preferentially bind to RAREs in cultured cells *in vivo* has been strongly supported by experiments described in Durand, B. *et al., Cell 71*:73-85 (1992).

As retinoic acid is known to regulate the proliferative and differentiative capacities of several mammalian cell types (Gudas, L.J. *et al.* (1994) In Sporn, M.B., Roberts, A.B. and Goodman, D.S.(eds), *The Retinoids.* 2nd edition, Raven Press, New York, pp. 443-520), retinoids are used in a variety of chemopreventive and chemotherapeutic settings. The prevention of oral, skin and head and neck cancers in patients at risk for these tumors has been reported (Hong , W. K. *et al., N. Engl. J. Med. 315*:1501-1505 (1986); Hong, W. K. *et al., N. Engl. J. Med. 323*:795-801 (1990); Kraemer, K. H. *et al., N. Engl. J. Med. 318*:1633-1637 (1988); Bollag, W. *et al., Ann. Oncol. 3*:513-526 (1992); Chiesa, F. *et al., Eur. J. Cancer B. Oral Oncol. 28*:97-102 (1992); Costa, A. *et al., Cancer Res. 54*:Suppl. 7, 2032-2037 (1994)), and retinoids are used in the therapy of acute promyelocytic leukemia (Huang, M.E. *et al., Blood 72*:567-572 (1988); Castaigne, S. *et al., Blood 76*:1704-1709 (1990); Chomienne, C. *et al., Blood 76*:1710-1717 (1990); Chomienne, C. *et al., J. Clin. Invest. 88*:2150-2154 (1991); Chen Z. *et al., Leukemia 5*:288-292 (1991); Lo Coco, F. *et al., Blood 77*:165701659 (1991); Warrell, R. P., Jr. *et al., N. Engl. J. Med. 324*:1385-1393 (1991)), squamous cell carcinoma of the cervix and the skin (Verma, A. K., *Cancer Res. 47*:5097-5101 (1987); Lippman S. M. *et al., J. Natl Cancer Inst. 84*:235-241 (1992); Lippman S. M. *et al., J. Natl Cancer Inst. 84*:241-245 (1992)) and Kaposi sarcoma (Bonhomme, L. *et al., Ann. Oncol. 2*:234-235 (1991)).

For example, in Chen, J-Y *et al., EMBO J. 14(6)*:1187-1197 (1995), a number of dissociating synthetic retinoids are characterized that selectively induce AF-2 activation function present in the LBD of RARβ (βAF-2). The authors also report that these synthetic retinoids, like RA, can inhibit the anchorage-independent growth of oncogene-transformed 3T3 cells. Further, the promoter of the human interleukin-6 (IL-6) gene, whose product is involved in the regulation of hematopoiesis, immune responses and inflammation (Kishimoto, T. *et al., Science 258*:593-597 (1992)), is induced by RA but not by the 'dissociating' retinoids which repressed its activity.

In addition to the retinoid receptors, compounds with agonistic and antagonistic properties on functions of the steroid receptors have also been reported. For example, in Meyer, M-E. *et al., EMBO J. 9(12)*: 3923-3932 (1990), a transient expression/gel retardation system was used to study the effects of RU486 and R5020 on glucocorticoid and progesterone receptor function. Further, in Halachimi, S., *et al., Science 264:*1455-1458 (1994), tamoxifen is shown to competitively inhibit estradiol-induced ERAP160 binding to the estrogen receptor, suggesting a mechanism for its growth-inhibitory effects in breast cancer. Accordingly, due to their clinical importance, there is great interest in developing screening methods capable of identifying agonist and antagonist of nuclear receptor transactivation.

As indicated, the present inventors have cloned a gene encoding TIF2 and have shown that TIF2 and a cytoplasmic fragment thereof bind, in an agonist-dependent manner, to all nuclear receptors analyzed— RAR, RXR, ER, TR, VDR, GR and AR. Further, the present inventors have shown that TIF2 polypeptides are transcriptional mediators of the nuclear receptor AF-2. Thus, the present invention further provides a screening method for identifying a nuclear receptor (NR) antagonist, which involves: (a) providing a host cell containing recombinant genes which express a polypeptide comprising a NR ligand binding domain (LBD) and a polypeptide comprising transcriptional intermediary factor-2 (TIF-2) or a TIF-2-fragment, wherein, in the presence of an agonist, said TIF-2 and said TIF-2-fragment bind said NR LBD; (b) administering a candidate antagonist to said cell; and (c) determining whether said candidate antagonist reduces either: (1) TIF-2- or TIF-2-fragment-binding to the AF-2 of said NR LBD as compared to said binding in the absence of said candidate antagonist; or (2) TIF-2- or TIF-2-fragment-stimulated NR LBD AF-2-mediated transactivation as compared to said transactivation in the absence of said candidate antagonist.

In a further aspect, a screening method is provided for identifying a nuclear receptor (NR) agonist, which involves: (a) providing a host cell containing recombinant genes which express a polypeptide comprising a NR ligand binding

domain (LBD) and a polypeptide comprising transcriptional intermediary factor-2 (TIF-2) or a TIF-2-fragment, wherein, in the presence of an agonist, said TIF-2 and said TIF-2-fragment bind said NR LBD; (b) administering a candidate agonist to said cell; and (c) determining whether said candidate agonist enhances either: (1) TIF-2- or TIF-2-fragment-binding to the AF-2 of said NR LBD as compared to said binding in the absence of said candidate agonist; or (2) TIF-2- or TIF-2-fragment-stimulated NR LBD AF-2-mediated transactivation as compared to said transactivation in the absence of said candidate agonist.

By "a host cell containing recombinant genes" is intended host cells into which one or more of the recombinant constructs described herein have been introduced or a progeny of such host cells.

Candidate antagonist and agonist according to the present invention include 'dissociating' ligands for nuclear receptors such as those described in Chen *et al., EMBO J. 14:*1187-1197 (1995) and Ostrowski *et al., Proc. Natl. Acad. Sci. USA 92:*1812-1816 (1995). Progesterone and glucocorticoid receptor agonist and antagonist are described in Meyer *et al., EMBO J. 9 (12):* 3923-3932 (1990). An estrogen receptor antagonist is described in Halachmi *et al., Science 264:*1455-1458 (1994). Thus, methods are known in the art for developing candidate nuclear receptor agonist and antagonist for screening according to the present invention. For example, the crystal structure of the ligand binding domains of certain nuclear receptors have been described. In particular, the crystal structure of the RXR LBD is described in Bourguet *et al., Nature 375:*377-382 (1995); the crystal structure of the RAR LBD is described in Renaud *et al., Nature 378:*681-689 (1995); and the crystal structure of a thyroid hormone receptor is described in Wagner *et al., Nature 378:*690-697 (1995). Using information from the crystal structure of a nuclear receptor, computer programs are available for designing the structure of candidate agonist and antagonist which would likely bind to the ligand binding domain. Suitable computer program packages for this purpose include WHAT IF (Vriend, G., *J. Mol. Graphics 8:*52-56 (1990)), and GRID (Goodford, *J. Med. Chem. 28:*849-857 (1985)).

Recombinant genes encoding a polypeptide comprising TIF2 or a TIF2-fragment capable of binding nuclear receptors in an agonist -dependent manner are described above. Recombinant genes encoding a polypeptide comprising a NR LBD have been described in great detail in the art. Methods for determining whether a candidate agonist or antagonist enhances or interferes with TIF-2 or TIF-2-fragment binding to a NR are known in the art. For example, the effect of a candidate agonist or antagonist on TIF2- or TIF-2-fragment-binding to a NR LBD can be studied using glutathione-S-transferase (GST) interaction assays by tagging NR LBDs with GST as described in detail in the Experimental section below and in Le Douarin *et al., EMBO J 14*:2020-2033 (1995).

Where the effect of a candidate agonist or antagonist on NR AF-2 transactivation is to be assayed, preferably, the recombinant genes will encode a chimeric polypeptide comprising a NR LBD fused to a DNA binding domain from a transactivator protein. In a further preferred embodiment, the host cell expressing the recombinant genes will also express a reporter gene. For example, in Chen *et al., EMBO J. 14(6):*1187-1197 (1995), three 'reporter' cell lines have been established in which RARα, RARβ, or RARγ agonists induce luciferase activity that can be measured in the intact cells using a single-photon-counting camera. These cell lines stably express chimeric proteins containing the DNA binding domain of the yeast transactivator GAL4 fused to the EF regions (which contain that LBD and the AF-2 activation function) of RARα (GAL-RARα), RARβ (GAL-RARβ) or RARγ (GAL-RARγ), and a luciferase reporter gene driven by a pentamer of the GAL4 recognition sequence ('17m') in front of the β-globin promoter (17mx5-G-Luc). This reporter system is insensitive to endogenous receptors which cannot recognize the GAL4 binding site. Further examples of reporter genes and reporter expression vectors for use according to the present invention to screen candidate agonist and antagonist of retinoid receptors are provided in Figure 6.

The ER expression vectors HEO, HE19 and HE15, the GR expression vectors HG1 and HG3 and the PR expression cPR1 and cPR3 are described in

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Kumar *et al., Cell 51:*941-951 (1987) and Gronemeyer *et al., EMBO J. 6:*3985-3994 (1987). The GR expression vector HG8 and the PR expression vector cPR5A are described in Bocquel *et al., Nucl. Acids Res. 17:*2581-2595 (1989). Reporter genes for the above described ER, GR and PR expression vectors include MMTV-CAT (in the case of PR and GR; Cato *et al., EMBO J. 5:*2237-2240 (1986)) and vit-tk-CAT (in the case of ER; Klein-Hitpass *et al., Cell 41:*1055-1061 (1986)).

The TR expression vector LexA-TR is described in Lee *et al., Nature 374:*91-94(1995), which also describes using the yeast two hybrid system to identify compounds that affect TR transactivation.

Still further references disclosing reporter plasmids containing a reporter gene and expression vectors encoding a NR LBD include Meyer *et al., Cell 57:*433-442 (1989); Meyer *et al., EMBO J. 9(12):*3923-3932 (1990); Tasset *et al., Cell 62:*1177-1187 (1990); Gronemeyer, H. and Laudet, V., *Protein Profile 2*:1173-1308 (1995); Webster *et al., Cell 54*:199-207 (1988); Strähle *et al., EMBO J. 7*:3389-3395 (1988); Seipel *et al., EMBO J. 11:*4961-4968 (1992); and Nagpal *et al., EMBO J. 12*:2349-2360 (1993). In a particularly preferred embodiment, the effect of a candidate agonist or antagonist on NR AF-2-mediated transactivation is assayed according to the method described in the legend to Figure 5 above.

The present inventors have identified an activation domain of TIF2, AD1 (amino acids 1010-1131 as shown in Figure 1 (SEQ ID NO:2)), which mediates the CBP-dependent transcriptional activation function of TIF2. Further, the present inventors have shown that polypeptides containing this activation domain, when fused to a DNA-binding domain of a transcriptional activator, is capable of activating transcription via a CBP-dependent pathway. Accordingly, the present invention further provides a screening method of identifying an agonist of TIF2 AD1 activation domain activity, which involves: (a) providing a host cell containing a recombinant gene or genes which express a polypeptide comprising a transcriptional activator DNA-binding domain (DBD) and a TIF-2 AD1

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activation domain 1; (b) administering a candidate agonist to said cell; and (c) determining whether said candidate agonist enhances TIF2 AD1 activation domain activity.

The invention further provides for a screening method for identifying an antagonist of TIF2 AD1 activation domain activity, which comprises: (a) providing a host cell containing a recombinant gene or genes which express a polypeptide comprising a transcriptional activator DNA-binding domain (DBD) and a TIF-2 AD1 activation domain 1; (b) administering a candidate antagonist to said cell; and (c) determining whether said candidate antagonist inhibits TIF2 AD1 activation domain activity.

By "transcriptional activator" it is meant molecules that enhance the initiation of transcription by RNA polymerase B (II). Transcriptional activators include yeast transcriptional activators, such as GAL4 and GCN4; the herpes simplex activator, VP16; and members of the nuclear receptor family, which includes RAR, RXR, ER, TR, VDR, GR, and AR.

Recombinant genes encoding a polypeptide comprising a TIF2 AD1 activation domain are described below. Recombinant genes encoding a polypeptide comprising a transcriptional activator DBD are well known in the art. Methods for determining whether a candidate agonist or antagonist enhances or interferes with transcription are well known in the art. For example, the effect of a candidate agonist or antagonist of TIF2 AD1 activation domain activity can be determined using CAT assays as described below and in Gronemeyer *et al.* (1987) and Bocquel *et al.*, *Nucl. Acids Res.* (1989).

Where the effect of a candidate agonist or antagonist of TIF2 AD1 activation domain activity is to be determined, preferably, recombinant genes will encode a chimeric polypeptide comprising a transcriptional activator DBD fused to a TIF2 polypeptide comprising the AD1 activation domain. In a further embodiment, the host cell expressing the recombinant genes will also express a reporter gene. Examples of reporter genes are described above. In a particularly preferred embodiment, the effect of a candidate agonist or antagonist of TIF2

AD1 activation domain function will be determined as described in the legend to Figure 7(c).

The present inventors have also identified a second activation domain of TIF2, AD2 (amino acids 1288-1464 as shown in Figure 1 (SEQ ID NO:2)), which mediates CBP-independent transcriptional activation. Further, the present inventors have shown that polypeptides containing this activation domain, when fused to a DNA-binding domain of a transcriptional activator, are capable of activating transcription via a CBP-independent pathway. Accordingly, the present invention further provides a screening method for identifying an agonist of TIF2 AD2 activation domain activity, which comprises: (a) providing a host cell containing a recombinant gene or genes which express a polypeptide comprising a transcriptional activator DNA-binding domain (DBD) and a TIF-2 AD2 activation domain; (b) administering a candidate agonist to said cell; and (c) determining whether said candidate agonist enhances TIF2 AD2 activation domain activity.

The invention further provides for a screening method for identifying an antagonist of TIF2 AD2 activation domain activity, which comprises: (a) providing a host cell containing a recombinant gene or genes which express a polypeptide comprising a transcriptional activator DNA-binding domain (DBD) and a TIF-2 AD2 activation domain; (b) administering a candidate antagonist to said cell; and (c) determining whether said candidate antagonist inhibits TIF2 AD2 activation domain activity.

Recombinant genes encoding a polypeptide comprising a TIF2 AD2 activation domain are described below. Recombinant genes encoding a polypeptide comprising a transcriptional activator DBD are well known in the art. Methods for determining whether a candidate agonist or antagonist enhances or interferes with transcription are known in the art.

Where the effect of a candidate agonist or antagonist of TIF2 AD2 activation domain activity is to be determined, preferably, recombinant genes will encode a chimeric polypeptide comprising a transcriptional activator DBD fused

to a TIF2 polypeptide comprising the AD2 activation domain. Transcriptional activators are described above. In a further embodiment, the host cell expressing the recombinant genes will also express a reporter gene. Examples of reporter genes are described above. In a particularly preferred embodiment, the effect of a candidate agonist or antagonist of TIF2 AD2 activation domain activity will be determined as described in the legend to Figure 7(c).

TIF-2 Antibodies and Methods

TIF2 antibodies are also provided by the present invention, as specific for a TIF2 protein, a TIF2 polypeptide, a TIF2 protein fragment or a TIF2 polypeptide fragment. The term "antibody" is meant to include polyclonal antibodies, monoclonal antibodies (mAbs), chimeric antibodies, anti-idiotypic (anti-Id) antibodies to antibodies that can be labeled in soluble or bound form, as well as fragments thereof provided by any known technique, such as, but not limited to enzymatic cleavage, peptide synthesis or recombinant techniques. Polyclonal antibodies are heterogeneous populations of antibody molecules derived from the sera of animals immunized with an antigen. A monoclonal antibody contains a substantially homogeneous population of antibodies specific to antigens, which population contains substantially similar epitope binding sites. MAbs may be obtained by methods known to those skilled in the art. See, for example Kohler and Milstein, Nature 256:495-497 (1975); U.S. Patent No. 4,376,110; Ausubel et al, eds., *CURRENT PROTOCOLS IN MOLECULAR BIOLOGY*, Greene Publishing Assoc. and Wiley Interscience, N.Y., (1987-1996); and Harlow and Lane *ANTIBODIES: A LABORATORY MANUAL* Cold Spring Harbor Laboratory (1988); Colligan et al., eds., *Current Protocols in Immunology*, Greene Publishing Assoc. and Wiley Interscience, N.Y., (1992-1996), the contents of which references are incorporated entirely herein by reference.

Such antibodies may be of any immunoglobulin class including IgG, IgM, IgE, IgA, GILD and any subclass thereof. A hybridoma producing a mAb of the present invention may be cultivated *in vitro*, *in situ* or *in vivo*. Production of high titers of mAbs *in vivo* or *in situ* makes this the presently preferred method of production.

Chimeric antibodies are molecules different portions of which are derived from different animal species, such as those having variable region derived from a murine mAb and a human immunoglobulin constant region, which are primarily used to reduce immunogenicity in application and to increase yields in production, for example, where murine mAbs have higher yields from hybridomas but higher immunogenicity in humans, such that human/murine chimeric mAbs are used. Chimeric antibodies and methods for their production are known in the art (Cabilly *et al., Proc. Natl. Acad. Sci. USA* 81:3273-3277 (1984); European Patent Application 125023 (published November 14, 1984); Neuberger et al., *Nature* 314:268-270 (1985); Taniguchi *et al.*, European Patent Application 171496 (1985); Morrison *et al.*, European Patent Application 173494 (1986); Neuberger *et al.*, PCT Application WO 86/01533, (1986); Kudo *et al.*, European Patent Application 184187 (1986); Morrison et al., European Patent Application 173494 (1986); Robinson et al., PCT Publication PCT/US86/02269 (1987); Liu *et al.*, *Proc. Natl. Acad. Sci. USA 84*:3439-3443 (1987); Sun *et al., Proc. Natl. Acad. Sci. USA 84*:214-218 (1987); Better *et al., Science 240*:1041- 1043 (1988); and Harlow and Lane, *ANTIBODIES: A LABORATORY MANUAL* Cold Spring Harbor Laboratory (1988)). These references are entirely incorporated herein by reference.

An anti-idiotypic (anti-Id) antibody is an antibody which recognizes unique determinants generally associated with the antigen-binding site of an antibody. An Id antibody can be prepared by immunizing an animal of the same species and genetic type (e.g., mouse strain) as the source of the mAb with the mAb to which an anti-Id is being prepared. The immunized animal will recognize and respond to the idiotypic determinants of the immunizing antibody by producing an antibody

to these idiotypic determinants (the anti-Id antibody). See, for example, U.S. patent No. 4,699,880, which is herein entirely incorporated by reference.

The anti-Id antibody may also be used as an "immunogen" to induce an immune response in yet another animal, producing a so-called anti-anti-Id antibody. The anti-anti-Id may be epitopically identical to the original mAb which induced the anti-Id. Thus, by using antibodies to the idiotypic determinants of a mAb, it is possible to identify other clones expressing antibodies of identical specificity. The anti-Id mAbs thus have their own idiotypic epitopes, or "idiotopes" structurally similar to the epitope being evaluated, such as GRB protein-α.

The term "antibody" is also meant to include both intact immunoglobulin molecules as well as fragments thereof, such as, for example, Fab and $F(ab')_2$, which are capable of binding antigen. Fab and $F(ab')_2$ fragments lack the Fc fragment of intact antibody, clear more rapidly from the circulation, and may have less non-specific tissue binding than an intact antibody (Wahl et al., J. Nucl. Med. 24:316-325 (1983)). It will be appreciated that Fab and $F(ab')_2$ and other fragments of the antibodies useful in the present invention may be used for the detection and quantitation of a TIF2 according to the methods disclosed herein for intact antibody molecules. Such fragments are typically produced by proteolytic cleavage, using enzymes such as papain (to produce Fab fragments) or pepsin (to produce $F(ab')_2$ fragments).

An antibody is said to be "capable of binding" a molecule if it is capable of specifically reacting with the molecule to thereby bind the molecule to the antibody. The term "epitope" is meant to refer to that portion of any molecule capable of being bound by an antibody which can also be recognized by that antibody. Epitopes or "antigenic determinants" usually consist of chemically active surface groupings of molecules such as amino acids or sugar side chains and have specific three dimensional structural characteristics as well as specific charge characteristics.

An "antigen" is a molecule or a portion of a molecule capable of being bound by an antibody which is additionally capable of inducing an animal to produce antibody capable of binding to an epitope of that antigen. An antigen may have one, or more than one epitope. The specific reaction referred to above is meant to indicate that the antigen will react, in a highly selective manner, with its corresponding antibody and not with the multitude of other antibodies which may be evoked by other antigens.

The antibodies, or fragments of antibodies, useful in the present invention may be used to quantitatively or qualitatively detect a TIF2 protein, polypeptide, or fragment, in a sample or to detect presence of cells which express a TIF2 of the present invention. This can be accomplished by immunofluorescence techniques employing a fluorescently labeled antibody (see below) coupled with light microscopic, flow cytometric, or fluorometric detection.

The antibodies (of fragments thereof) useful in the present invention may be employed histologically, as in immunofluorescence or immunoelectron microscopy, for *in situ* detection of a TIF2 protein, polypeptide, or fragment, of the present invention. In situ detection may be accomplished by removing a histological specimen form a patient, and providing a labeled antibody of the present invention to such a specimen. The antibody (or fragment) is preferably provided by applying or by overlaying the labeled antibody (or fragment) to a biological sample. Through the use of such a procedure, it is possible to determine not only the presence of a TIF2 protein, polypeptide, or fragment, but also its distribution on the examined tissue. Using the present invention, those of ordinary skill will readily perceive that any of wide variety of histological methods (such as staining procedures) can be modified in order to achieve such in situ detection.

Such assays for a TIF2 protein, polypeptide, or fragment, of the present invention typically comprises incubating a biological sample, such as a biological fluid, a tissue extract, freshly harvested cells such as lymphocytes or leukocytes, or cells which have been incubated in tissue culture, in the presence of a detectably

labeled antibody capable of identifying a TIF2 protein, polypeptide, or fragment, and detecting the antibody by any of a number of techniques well-known in the art.

The biological sample may be treated with a solid phase support or carrier such as nitrocellulose, or other solid support or carrier which is capable of immobilizing cells, cell particles or soluble proteins. The support or carrier may then be washed with suitable buffers followed by treatment with a detectably labeled TIF2-specific antibody. The solid phase support or carrier may then be washed with the buffer a second time to remove unbound antibody. The amount of bound label on said solid support or carrier may then be detected by conventional means.

By "solid phase support", "solid phase carrier", "solid support", "solid carrier", "support" or "carrier" is intended any support or carrier capable of binding antigen or antibodies. Well-known supports or carriers, include glass, polystyrene, polypropylene, polyethylene, dextran, nylon amylases, natural and modified celluloses, polyacrylamides, gabbros, and magnetite. The nature of the carrier can be either soluble to some extent or insoluble for the purposes of the present invention. The support material may have virtually any possible structural configuration so long as the coupled molecule is capable of binding to an antigen or antibody. Thus, the support or carrier configuration may be spherical, as in a bead, or cylindrical, as in the inside surface of a test tube, or the external surface of a rod. Alternatively, the surface may be flat such as a sheet, test strip, etc. Preferred supports or carriers include polystyrene beads. Those skilled in the art will know many other suitable carriers for binding antibody or antigen, or will be able to ascertain the same by use of routine experimentation.

The binding activity of a given lot of anti-TIF2 antibody may be determined according to well known methods. Those skilled in the art will be able to determine operative and optimal assay conditions for each determination by employing routine experimentation. Other such steps as washing, stirring,

shaking, filtering and the like may be added to the assays as is customary or necessary for the particular situation.

One of the ways in which a TIF2-specific antibody can be detectably labeled is by linking the same to an enzyme and use in an enzyme immunoassay (EIA). This enzyme, in turn, when later exposed to an appropriate substrate, will react with the substrate in such a manner as to produce a chemical moiety which can be detected, for example, by spectrophotometric, fluorometric or by visual means. Enzymes which can be used detectably label the antibody include, but are not limited to, malate dehydrogenase, staphylococcal nuclease, delta-5-steroid isomerase, yeast alcohol dehydrogenase, alpha-glycerophosphate dehydrogenase, triose phosphate isomerase, horseradish peroxidase, alkaline phosphatase, asparaginase, glucose oxidase, beta-galactosidase, ribonuclease, urease, catalase, glucose-6- phosphate dehydrogenase, glucoamylase and acetylcholinesterase. The detection can be accomplished by colorimetric methods which employ a chromogenic substrate for the enzyme. Detection may also be accomplished by visual comparison of the extent of enzymatic reaction of a substrate in comparison with similarly prepared standards.

Detection may be accomplished using any of a variety of other immunoassays. For example, by radioactivity labeling the antibodies or antibody fragments, it is possible to detect R-PTPase through the use of a radioimmunoassay (RIA). A good description of RIA maybe found in Laboratory Techniques and Bio chemistry in Molecular Biology, by Work, T.S. et al., North Holland Publishing Company, NY (1978) with particular reference to the chapter entitled "An Introduction to Radioimmune Assay and Related Techniques" by Chard, T., incorporated by reference herein. The radioactive isotope can be detected by such means as the use of a γ counter or a scintillation counter or by autoradiography.

It is also possible to label an anti-TIF2 antibody with a fluorescent compound. When the fluorescently labeled antibody is exposed to light of the proper wave length, its presence can be then be detected due to fluorescence.

Among the most commonly used fluorescent labeling compounds are fluorescein isothiocyanate, rhodamine, phycoerythrin, phycocyanin, allophycocyanin, o-phthaldehyde and fluorescamine.

The antibody can also be detectably labeled using fluorescence emitting metals such as ^{152}EU, or others of the lanthanide series. These metals can be attached to the antibody using such metal chelating groups as diethylenetriamine pentaacetic acid (EDTA).

The antibody also can be detectably labeled by coupling it to a chemiluminescent compound. The presence of the chemiluminescent-tagged antibody is then determined by detecting the presence of luminescence that arises during the course of a chemical reaction. Examples of particularly useful chemiluminescent labeling compounds are luminol, isoluminol, theromatic acridinium ester, imidazole, acridinium salt and oxalate ester.

Likewise, a bioluminescent compound may be used to label the antibody of the present invention. Bioluminescence is a type of chemiluminescence found in biological systems in which a catalytic protein increases the efficiency of the chemiluminescent reaction. The presence of a bioluminescent protein is determined by detecting the presence of luminescence. Important bioluminescent compounds for purposes of labeling are luciferin, luciferase and aequorin.

An antibody molecule of the present invention may be adapted for utilization in a immunometric assay, also known as a "two-site" or "sandwich" assay. In a typical immunometric assay, a quantity of unlabeled antibody (or fragment of antibody) is bound to a solid support or carrier and a quantity of detectably labeled soluble antibody is added to permit detection and/or quantitation of the ternary complex formed between solid-phase antibody, antigen, and labeled antibody.

Typical, and preferred, immunometric assays include "forward" assays in which the antibody bound to the solid phase is first contacted with the sample being tested to extract the antigen form the sample by formation of a binary solid phase antibody-antigen complex. After a suitable incubation period, the solid

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support or carrier is washed to remove the residue of the fluid sample, including unreacted antigen, if any, and then contacted with the solution containing an unknown quantity of labeled antibody (which functions as a "reporter molecule"). After a second incubation period to permit the labeled antibody to complex with the antigen bound to the solid support or carrier through the unlabeled antibody, the solid support or carrier is washed a second time to remove the unreacted labeled antibody.

In another type of "sandwich" assay, which may also be useful with the antigens of the present invention, the so-called "simultaneous" and "reverse" assays are used. A "simultaneous" and "reverse" assays are used. A simultaneous assay involves a single incubation step as the antibody bound to the solid support or carrier and labeled antibody are both added to the sample being tested at the same time. After the incubation is completed, the solid support or carrier is washed to remove the residue of fluid sample and uncomplexed labeled antibody. The presence of labeled antibody associated with the solid support or carrier is then determined as it would be in a conventional "forward" sandwich assay.

In the "reverse" assay, stepwise addition first of a solution of labeled antibody to the fluid sample followed by the addition of unlabeled antibody bound to a solid support or carrier after a suitable incubation period is utilized. After a second incubation, the solid phase is washed in conventional fashion to free it of the residue of the sample being tested and the solution of unreacted labeled antibody. The determination of labeled antibody associated with a solid support or carrier is then determined as in the "simultaneous" and "forward" assays.

Having generally described the invention, the same will be more readily understood by reference to the following examples, which are provided by way of illustration and are not intended as limiting.

Example 1: TIF2 Cloning and Expression

In keeping with previous reports (Halachmi, S. *et al., Science 264*:1455-1458 (1994); Cavaillès, V. *et al., Proc. Natl. Acad. Sci. USA 91*:10009-10013 (1994); Kurokawa, R. *et al, Nature 377*:451-454 (1995)), we observed agonist-dependent binding *in vitro* of a 160-kDa protein from ^{35}S-labelled whole cell extracts (HeLa, Cos-1, P19.6, MCF-7) to the glutathione-S-transferase (GST)-tagged LBDs of retinoic acid (RAR) and estrogen (ER) receptors (FIG. 2a). One cDNA clone, identified by screening 340,000 clones of a human placenta cDNA expression library with an estradiol (E2)-bound ^{32}P-labelled ER(DEF) probe, encoded a protein fragment (TIF2.1) that interacted on Far-Western blots with three different ^{32}P-labelled NR LBDs (ER, RAR, RXR) in an agonist-dependent manner (not shown), and could therefore correspond to the above 160-kDa protein. The TIF2 coding sequence (FIG. 3a), preceded by in-frame stop codons 5′ of the initiator AUG, was obtained upon rescreening with a TIF2.1 cDNA probe. Human TIF2 cDNA encodes a 159,160 Da protein (1,464 amino acids), which includes N-terminal putative nuclear localization signals (NLSs), one Gln- and three Ser/Thr-rich regions, and two charged clusters (FIG. 3). Some regions of TIF2 show significant sequence similarities with the recently described (Onate, S.A. *et al., Science 270*:1354-1357 (1995)) steroid receptor coactivator SRC-1 (FIG. 3). TIF2 appears to be widely expressed, since the corresponding transcript was found in several human tissues, albeit at a much lower level in kidney (FIG. 2c and not shown).

Immunodepletion studies strongly support that TIF2 is the 160-kDa protein species which interacts in an agonist-dependent manner with NR LBDs (see above and Halachmi, S. *et al., Science 264*:1455-1458 (1994); Cavaillès, V. *et al., Proc. Natl. Acad. Sci. USA 91*:10009-10013 (1994); and Kurokawa, R. *et al, Nature 377*:451-454 (1995)). Western blotting with a rabbit antiserum (pα-TIF2), raised against bacterially expressed TIF2.1, revealed predominantly a 160-kDa HeLa cell protein that interacted with agonist-bound GST-ER(DEF) (FIG.

2b, lanes 1 and 2; see also legend to FIG. 2b). Immunodepletion with a mouse monoclonal TIF2 antibody (mα-TIF2) prior to affinity purification resulted in a specific decrease of TIF2, but not TIF1 (Le Douarin, B. *et al., EMBO J. 14*:2020-2033 (1995)) amounts, retained on E2-bound GST-ER(DEF) (FIG. 2b, compare lanes 2 with 4 and 6 with 8). Importantly, the subsequent Far-Western analysis with an E2-bound ^{32}P-GST-ER(DEF) probe revealed the 160-kDa species only in control, but not TIF2-immunodepleted extracts (FIG. 2b, compare lanes 10 and 12).

Transiently expressed full-length TIF2 was nuclear and mainly associated with discrete bodies (FIG. 4a). Since the overexpressed TIF2.1 fragment was essentially cytoplasmic (supporting the above assignment of a N-terminal TIF2 NLS), the interaction of TIF2.1 with NRs could be studied in mammalian cells using nuclear cotranslocation assays. In the absence of ligand, TIF2.1 remained cytoplasmic and NRs were nuclear (for RARα, ER and PR, see FIGs. 4b, d, g). Agonist exposure, however, resulted in all three cases in nuclear colocalization of TIF2.1 and NR, indicating NR-TIF2 interaction *in vivo* (FIGs. 4c, e, h). Agonist-dependent interaction of TIF2.1 with NRs was observed for all other receptors analyzed (RXR, TR, VDR, GR and AR; not shown). Interestingly, no interaction was detected between ER and TIF2.1 in presence of the ER AF-2 antagonist hydroxytamoxifen (OHT) (FIG. 4f), and the PR AF-2 antagonist RU 486 reversed the R5020-induced PR-TIF2.1 interaction (FIG. 4i).

In agreement with the Far-Western blot experiments NRs and TIF2 directly interacted, as purified TIF2.1 protein bound *in vitro* in the presence of an agonist to GST-ER(DEF), GST-RARα(DEF), GST-RXRα(DE) and GST-TR(DE) (FIG. 4k, l, m, lanes 3 and 4; FIG. 4n, lanes 5 and 6). As expected, TIF2 binding to GST-RXRα(DE) occurred with 9*cis*-RA (9C-RA) but not all -*trans*-RA (T-RA) (FIG. 4n, lanes 1 and 2), and OHT prevented E2-dependent binding of TIF2 to GST-ER(DEF) (FIG. 4n, lanes 7-9). The integrity of the conserved core of the ER, RARα and RXRα AF-2 activating domains (AF-2 AD) which was shown to be critical for AF-2 activity (Le Douarin, B. *et al., EMBO J.*

14:2020-2033 (1995); Danielian, P.S. *et al., EMBO J. 11*:1025-1033 (1992); Durand, B. *et al., EMBO J. 13*:5370-5382 (1994); and Gronemeyer, H. and Laudet, V., *Protein Profile 2*:1173-1308 (1995), and therein), was required for TIF2 interaction *in vitro*. Most AF-2 AD core mutants which have lost AF-2 activity (ER, FIG. 4k, lanes 5-8; RARα, FIG. 4l, lanes 5-10; RXRα, FIG. 4m, lanes 5-8) did not detectably, or only weakly, associate with TIF2, whereas the GST-LBD fusion of the RXRα mutant E461Q, whose AF-2 is only partially impaired (Le Douarin, B. *et al., EMBO J. 14*:2020-2033 (1995)), still exhibited a significant RA-dependent interaction with TIF2.1 *in vitro* (FIG. 4m, lanes 9 and 10). No significant interaction of TIF2.1 was observed with either GST-VP16 (acidic activation domain), GST-TBP, GST-TFIIB, or a series of GST-TAFs ($hTAF_{II}18$, $hTAF_{II}20$, $hTAF_{II}28$ and $hTAF_{II}55$; see Jacq, X. *et al., Cell 79*:107-117 (1994); Mengus, G. *et al., EMBO J. 14*:1520-1531 (1995)) (not shown).

Conceptually, a TIF capable of mediating the transcriptional activity of a cognate AF to the transcription machinery, could itself be an activator when fused to a heterologous DNA-binding domain. Interestingly, in transiently transfected HeLa cells, TIF2.1 fused to the GAL4 DNA-binding domain strongly transactivated a GAL4 reporter (FIG. 5a). Thus, TIF2 may correspond to one of the hypothetical limiting factor(s) previously proposed to be involved in NR transcriptional interference/squelching (Meyer, M.-E. *et al., Cell 57*:433-442 (1989); Bocquel, M.-T. *et al., Nucl. Acids Res. 17*:2581-2595 (1989); Tasset, D. *et al., Cell 62*:1177-1187 (1990)). Supporting this possibility, "anti-squelching" experiments showed that expression of TIF2.1 in ER-transfected cells could, at least partially, reverse the transcriptional autointerference (Bocquel, M.-T. *et al., Nucl. Acids Res. 17*:2581-2595 (1989)) generated by expressing increased amounts of ER (FIG. 5b; note the marked shift of the bell-shaped activation curve to higher ER concentrations in the presence of TIF2.1). At high ER expression levels, the TIF2.1-stimulated transactivation decreased, possibly due to squelching of other putative mediators (Jacq, X. *et al., Cell 79*:107-117 (1994); Lee, J.W. *et al., Nature 374*:91-94 (1995); Le Douarin, B. *et al., EMBO J. 14*:2020-2033

(1995); vom Baur, E. *et al., EMBO J. 15*:110-124 (1996); Lee, J.W. *et al., Endocrinology 9*:243-254 (1995); Cavaillès, V. *et al., EMBO J. 14*:3741-3751 (1995); Onate, S.A. *et al., Science 270*:1354-1357 (1995)) and/or transcriptional factors.

As expected, coexpression of TIF2.1 with antagonist-bound NR did not lead to any stimulation of the transactivation brought about by AF-1 in the presence of pure AF-2 antagonists (Berry, M. *et al., EMBO J. 9*:2811-2818 (1990); Meyer, M.E. *et al., EMBO J. 9*:3923-3932 (1990)), further supporting that TIF2 is AF-2-specific (FIG. 5b and 5e for ER, OHT; FIG. 5d for PR, RU486). TIF2 expression also increased AF-2/agonist-mediated transactivation by the androgen (AR) and progesterone (PR) receptors, but not transactivation by GAL-VP16 and GAL-AP2 (FIG. 5c). Under similar conditions, transactivation by GAL-RAR, GAL-RXR, GAL-VDR, GAL-TR and GAL-GR were unaffected by TIF2 (FIG. 5c, and not shown), suggesting that for these NRs either TIF2 is not critically involved in mediating their AF-2 activities or endogenous TIF2 amounts are sufficient to optimally support transactivation, for instance, because TIF2 has a higher affinity for these receptors. TIF2-stimulation is to some extent affected by the promoter environment of the responsive gene, as the TIF2 effect on PR/5020-induced transactivation was greater for a complex (MMTV) than for a minimal (GRE-TATA) promoter, although the latter was also reproducibly stimulated (FIG. 5d). As expected from the distinct levels of TIF2 transcripts in different tissues (FIG. 2c), the effect of TIF2 was cell type-dependent, since TIF2 had a much stronger effect on PR- and ER-induced transactivations in Cos-1 than in HeLa cells (FIGs. 5d, e).

Squelching (Meyer, M.-E. *et al., Cell 57*:433-442 (1989); Bocquel, M.-T. *et al., Nucl. Acids Res. 17*:2581-2595 (1989); Tasset, D. *et al., Cell 62*:1177-1187 (1990)) and structural studies (Bourguet, M. *et al., Nature 375*:377-382 (1995); Benaud, J.-P. *et al., Nature 378*:681-689 (1995); Wagner, R.L. *et al., Nature 378*:690-697 (1995); Wurtz, J.-M. *et al., Nature Struct. Biol. 3*:87-94 (1996)) have supported a model in which binding of the ligand to the LBD of NRs

results in conformational changes generating the surface(s) required for interaction with transcriptional intermediary factors (TIFs/mediators) which transduce the AF-2 activity to the transcription machinery. Conceptually such mediators should exhibit the following properties: (i) they should bind to agonist-, but not antagonist-bound NR LBDs, (ii) their binding should be prevented by mutations abolishing AF-2 activity, (iii) they should collectively exhibit a transactivation function(s), (iv) their expression should relieve AF-2 autosquelching, and (v) their overexpression should stimulate the activity of AF-2, whenever they are present in limiting amounts. The present study is the first report of a *bona fide* mediator of NR AF-2s which exhibits all these properties.

Example 2: Production of TIF-2 Antibodies

The following TIF2 antibodies were made using known techniques, unless otherwise specified below. *See, e.g.,* Ausubel et al, eds., *CURRENT PROTOCOLS IN MOLECULAR BIOLOGY*, Greene Publishing Assoc. and Wiley Interscience, N.Y., (1987-1996); Harlow and Lane *ANTIBODIES: A LABORATORY MANUAL* Cold Spring Harbor Laboratory (1988); and Colligan et al., eds., *Current Protocols in Immunology*, Greene Publishing Assoc. and Wiley Interscience, N.Y., (1992-1996), the contents of which references are incoporated entirely herein by reference.

Polyclonal Antibodies. The TIF2.1 coding sequence (amino acids 624-1287) was cloned into pET15b and the resulting plasmid transformed into the *E. coli* strain BL21 (DE3). After overexpression of the $(His)_6$-TIF2.1 protein the bacteria were lysed and the protein purified from the crude extract via affinity chromatography on a HiTrap chelating column (Pharmacia) as described (see Bourguet *et al., Prot. Expr. Purif.* 6:604-608 (1995) for technical details). Aliquots of the purified protein (50μg) in emulsion (Freund's Adjuvant) were injected (only once) into a New Zealand rabbit using a multisite intradermal injection protocol. Antisera obtained from serial bleeds revealed a single band of

about 160 kDa on Western blots of extracts from Cos-1 cells transformed with a full length TIF2 expression vector.

Monoclonal Antibodies. A 20mer amino-acid peptide of TIF2 (with an added C-terminal cysteine) was selected on the basis of its potential immunogenic characteristics in terms of hydrophilicity, flexibility, surface probability and the 'antigenic index' according to software programmes Plot and Peptidestructure from the GCG package.

The chosen peptide corresponds to the N terminal fragment encoded by the TIF2 partial cDNA initially isolated (which encodes amino acids 624 to 1287) and corresponds to amino acids 624 to 643 of the total protein (SEQ ID NO:2):

ERADGQSRLHDSKGQTKLLQ(C) (SEQ ID NO:4)
624 643

The peptide was coupled to ovalbumin via the additional cysteine using the MBS heterobifunctional crosslinker. Injections were performed in BALB/c mice intraperitonally and intravenously.

Spleen cells from the immunized mice were fused to the Sp2/0 Ag14 myeloma. Growing hybridomas were first screened by ELISA using the recombinant TIF2.1 protein and the free peptide. Positive cultures were then tested by immunocytofluorescence on Cos cells transfected with TIF2.1 (in the pSG5 vector) as well as by western blot using the transfected Cos cell extracts and HeLa nuclear extract. The positive cultures were also tested for their ability to immunoprecipitate the TIF2.1 protein from Cos transfected cells.

Cultures were cloned twice on soft agar. 5 hybridomas have been established, 4 secreting IgG_1, κ and 1 IgG_{2a}, κ antibodies, as shown in the Table:

Hybridoma	ELISA	Immuno fluoresc. (Cos)	Western blot. (Cos)	Immuno precip. (Cos)
1Ti-1B6 (IgG_1, κ)	+	+	+	+
1Ti-1C9 (IgG_1, κ)	+	+	+	-
1Ti-1D8 (IgG_1, κ)	+	+	++	+
1Ti-1D12 (IgG_1, κ)	+	+	++	+
1Ti-1G3 (IgG_{2a}, κ)	+	+	++	+

Example 3: Identification of TIF2 NID

All recombinant DNA work was performed according to standard procedures (Ausubel, F.M. *et al., Current Protocols in Molecular Biology*, John Wiley & Sons, New York (1993)). GST-fusions of nuclear receptors were expressed from the following previously described plasmids: GST (pGEX2T; Pharmacia), GST-ER (pGEX2T-hERα(DEF), also called pGEX2THE14G, amino acids 282-595), GST-RXR (pGEX2T-mRXRα(DE), amino acids 205-467), and GST-RAR (pGEX2T-hRARα(DEF), amino acids 153-462) (all LeDouarin, B. *et al., EMBO J. 14*:2020-2033 (1995a)).

To further delineate the TIF2 NR interaction domain (NID), we studied the interaction between a series of TIF2 deletion mutants and the ER or RARα LBDs, using GST-fusion protein-based *in vitro* assays. In both cases, an NID was mapped to the central region of TIF2 (amino acids 624-869 in mutant TIF2.5; see FIGS. 7a and b). No additional NID could be identified in the N- or C-termini of TIF2 (FIGS. 7a and b; mutants TIF2.0, TIF2.2 and TIF2.7). Note that, in contrast, SRC-1, a paralogue of TIF2, apparently harbours two distinct non-contiguous NIDs located in the central and C-terminal regions (Oñate, S.A. *et al.*,

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Science 270:1354-1357 (1995); Yao, T.P. *et al., Proc. Natl. Acad. Sci. USA 93*:10626-10631 (1996); Zhu, Y. *et al., Gene Expression 6*:185-195 (1996)).

To further narrow down the TIF2 NID, TIF2.5 was C-terminally truncated to Pro775, yielding TIF2.34 which also interacted with ER and RARα LBDs in a ligand-dependent manner (FIGS. 8a and c). Upon further truncation to Ser697, the resulting mutant still interacted with both ER and RARα LBDs but, surprisingly, a ligand-dependent interaction was also found with TIF2.36 (FIGS. 8a and c), thus indicating that the TIF2 NID is composed of at least two autonomous NO-interacting modules.

An alignment of the TIF2 NID amino acid sequence present in TIF2.34 with the corresponding region of SRC-1 (Oñate, S.A. *et al., Science 270*:1354-1357 (1995)) revealed three highly conserved regions (FIG. 8a). Interestingly, all three contain the motif LxxLL (SEQ ID NO:12)(FIG. 8b), originally identified in the so-called "nuclear receptor box" (NR box) of TIFlα as the LxxLLL (SEQ ID NO:13) motif, which was also present in RIP140 (Cavaillès, V. *et al., EMBO J. 14*:3741-3751 (1995)) and TRIP3 (Lee, J.W. *et al.*,(1995)) (see LeDouarin, B. *et al., EMBO J. 15*:6701-6715 (1996) and FIG. 8b). Importantly, 10-amino-acid sequences comprising the TIFlα or RP140 NR boxes were sufficient for functional interaction with RXR in a ligand- and AF-2 AD-integrity-dependent manner, and mutation of the leucines at position 4 and 5 (LL→AA) of the TIFlα LxxLLL (SEQ ID NO:13) motif abrogated TIFlα-RXR interaction (LeDouarin, B. *et al., EMBO J. 15*:6701-6715 (1996)). The functionality of the RIP140 NR box was recently confirmed (Heery, D.M. *et al., Nature 387*:733-736 (1997)).

To investigate the functional significance of these three motifs in the TIF2 NID, the above LL→AA mutation was introduced in TIF2.1, either into each motif alone or in all possible combinations of the three motifs (TIF2.lml to ml23 in FIG. 8a; numbers following "m" refer to the mutated motifs). Mutation of all three MR boxes was required to abrogate both the binding to ER, RARα and RXRα (FIG. 8d, quantitation in FIG. 8e, white bars) and TIF2-dependent stimulation of ligand-induced transactivation by ER and RXRα AF-2s (FIG. 8e,

black bars, and data not shown; in the case of RARα AF-2 the stimulation was weak and was not quantified). TIF2.1 constructs in which two NR box motifs were mutated still exhibited ER binding and stimulation of AF-2 activity, in particular when the NR box motif II was intact, suggesting that the three NR box-containing modules are at least in part, functionally redundant (FIGS. 8d and e; TIF2.1m12, m13, and m23). This redundancy was obvious when only one NR box motif was mutated; in contrast to TIFlα, which contains only one NR box (LeDouarin, B. *et al., EMBO J. 15:*6701-6715 (1996)), mutation of a single TIF2 NR box did not abrogate ER binding and stimulation of ER AF-2 activity. All three mutants (TIF2.1m1 to m3) bound to ER and stimulated estradiol-dependent transactivation by the ER with similar efficiency as TIF2.1 itself (FIGS. 8d and e). In the case of RARα and RXRα the mutations had, in general, a more deleterious effect on receptor LBD binding and stimulation of AF-2 activity than in the case of ER (FIGS. 8d and e). This may possibly reflect a weaker interaction between TIF2 and either RARα or RXRα than with ER. However, in spite of exhibiting in general a lower activity, the patterns of NR binding and stimulation of AF-2 activity of the NR box mutants were similar for ER and RARα and RXRα, as mutation of motif II was always more detrimental in double mutants than mutation of motifs I and III (see FIG. 8e). Importantly, for both ER and RXRα there was a good correlation between the effect of any of the various mutations on TIF2.1-receptor binding *in vitro* and TIF2.1-mediated stimulation of AF-2 activity (FIG. 8e), supporting a mechanism whereby the stimulation of AF-2 activity by TIF2 involves TIF2-NO interaction through NR holo-LBD-TIF2 NR box interface(s).

Our present structure-function analysis reveals that TIF2 contains a single nuclear receptor-interaction domain (NID). Note in contrast to the other TIF2 family member, SRC-1, which was reported to contain two NIDs (Oñate, S.A. *et al., Science 270:*1354-1357 (1995); Yao, T.P. *et al., Proc. Natl. Acad. Sci. USA 93:*10626-10631 (1996); Zhu, Y. *et al., Gene Expression 6:*185-195 (1996)). Note, however, that one of the two SRC-1 NID is most probably homologous to

the TIF2 NID characterized here (see FIG. 8a). The TIF-2 NID is composed of three modules, and each can bind independently in a ligand-dependent manner to the NRs tested in this study. Interestingly, these modules contain the NR box motif LxxLL (SEQ ID NO:12), which was originally recorded (as the motif LxxLLL (SEQ ID NO:13), FIG. 8b) within a 10 amino acid NR binding module of TIF1α which was found to be conserved in the NID of RIP140 and also present in TRIP3 (LeDouarin, B. *et al., EMBO J. 15:*6701-6715 (1996) and refs therein). Moreover, the TIF1α and RIP140 modules were shown to functionally interact with NRs (LeDouarin, B. *et al., EMBO J. 15:*6701-6715 (1996)). The implication of NR box motifs in NO-coactivator binding and their presence in a number of different coactivators was pointed out in recent reports (Heery, D.M. *et al., Nature 387*:733-736 (1997); Torchia, J. *et al., Nature 387*:677-684 (1987); LeDouarin, B. *et al., EMBO J. 15:*6701-6715 (1996)). Note that all three TIF2 NR box motifs described here are conserved in the recently discovered TIF2 paralogue p/CIP (Torchia, J. *et al., Nature 387*:677-684 (1987)). In contrast to TIF1α, for which mutation of leucines at positions 4 and 5 to alanine of its single NR box motif (LL→AA) abrogates NR binding, mutation of all three motifs are required in the TIF2 NID to abrogate NR binding, indicating that each of these motifs can contribute to a TIF2 surface that interacts with a cognate surface of NR holo-LBDs. That the NR boxes of TIF2 exhibit functional redundancy is supported by the observation that the LL→AA mutation in any of the three TIF2 NID motifs apparently did not (in the case of the ER) or only weakly (in the case of RARα, RXRα) reduce the efficiency of NR interaction. Moreover, in the TIF2.1 environment, any single intact NR box motif on its own (i.e., when the two other motifs were mutated) was sufficient for interaction with the holo-ER LBD, although only motif II on its own could bring about a nearly wild-type NR binding efficiency. In contrast, for RARα and RXRα interaction, mutants with single intact NR boxes were 5 (box II) to 20 (box I or III) times less efficient than the wild-type TIF2 containing the three NR boxes. Crystallography studies will be necessary to distinguish between two possible models, in which the three NR box

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motifs (i) contribute to the formation of a tripartite NID surface that specifically recognizes a cognate holo-NO LBD surface, or (ii) belongs to independent surfaces which each can interact, albeit with different efficiencies, with the same holo-NO surface. Note, however, that the second model could allow TIF2 to interact cooperatively with both partners of NR homo- or heterodimers, thus rendering transactivation by NRs sensitive to small variations in TIF2 levels. Note also that, for both ER and RXRα, the effects of NR box mutations on NR binding and stimulation of AF-2 activity were correlated, further supporting the conclusion that the transcriptional effect of TIF2 involves the formation of a NR box-NO LBD interaction interface.

The motif LxxLL (SEQ ID NO:12) has been found in a number of other NR coactivators (see above), thus suggesting some similarity in the mode of NO-coactivator interactions. However, this does not exclude NO-specific modulation of these interactions, as the NR box surrounding sequences are highly variable. In this respect, note also that TIF2 NR boxes II and III are predicted to form α-helices, while NR box I is predicted to fold into a β-sheet structure (structure predictions according to SOPMA; Geourjon and Deleage, 1994).

Example 4: Identification of the AD1 and AD2 activation domains of TIF2

Transient transfection assays with a GAL4 reporter plasmid and chimeras containing various TIF2 fragments linked to the GAL4 DNA binding domain (DBD) demonstrated the presence of two autonomous transcriptional activation domains in the C-terminal 460 amino acids of TIF2, termed AD1 and AD2 (delineated by mutants TIF2.8, TIF2.12 and TIF2.2 in FIGS. 7a and c). Transient transfections of HeLa and Cos-1 cells were performed as described (Gronemeyer *et al.*, (1987); Bocquel, M.T. *et al., Nucl. Acids Res. 17*:2581-2595 (1989)).

The N-terminal AD1 (amino acids 1010-1131), which is present in TIF2.1, showed a stronger activity than the C-terminal AD2 (amino acids 1288-1464) (compare TIF2.8 and TIF2.12 with TIF2.2 in FIGS. 7a and c). Note, however,

that the weaker activity of AD2 (relative to AD1) could be due to a lower expression level of the GAL-TIF2.2 fusion protein (compare with GAL-TIF2.8 and GAL-TIF2.12 in FIG. 7c). Both TIF2 activation functions were active in Cos-1 and HeLa cells (FIG. 7c). Notably, the minimal AD1 (TIF2.8) and AD2 (TIF2.2) constructs exhibited some cell-specific activities, as GALTIF2.8 was more active in HeLa than in Cos cells, whereas the opposite was observed for GAL-TIF2.2 (FIG. 7c). Interestingly, the glutamine-rich region of TIF2 could neither activate transcription on its own when fused to the GAL4 DBD (FIGS. 7a and c; mutant TIF2.6), nor was it required for transcriptional activation by AD1 or AD2. No activation function could be detected in the N-terminal part of TIF2 (see FIGS. 7a and c; mutant TIF2.0).

We conclude from these data that the nuclear receptor interacting domain (NID) and the two transcriptional activation functions of TIF2 correspond to distinct modular domains, since TIF2.5 can bind to NRs, but cannot activate transcription, whereas TIF2.2 and TIF2.8 cannot bind NRs but are able to activate transcription (FIG. 7a).

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Example 5: Characterization of the TIF2 AD1 and AD2 activation domains

Recently CBP and p300, originally identified as coactivators of the transcription factor CREB, were shown to act as general integrators of multiple signaling pathways, including activation via agonist-bound RARα and TR (for reviews and refs see Eckner, R., *Biol. Chem. 377*:685-688 (1996); Janknecht & Hunter,(1996); Glass, C.K. *et al., Current Opin. Cell Biol. 9*:222-232 (1997); Shikama, N. *et al., Trends in Cell Biol. 7*:230-236 (1997)). Furthermore, it was reported that SRC-1, which belongs to the same gene family as TIF2, interacts with CBP and p300 (Kamei, Y. *et al., Cell 85*:403-414 (1996); Yao, T.P. *et al., Proc. Natl. Acad. Sci. USA 93*:10626-10631 (1996); Hanstein, B., *et al., Proc. Natl. Acad. Sci USA 93*:11540-11545 (1996)). Using GST-fusion protein-based

interaction and animal cell-based two hybrid assays, we therefore analyzed whether TIF2 could also interact with CBP. In the two hybrid system only the central TIF2.1 fragment, but not the N-terminal TIF2.0 or the C-terminal TIF2.2 fragments (FIG. 7a), scored positive for interaction with GAL-CBP (containing amino acids 1872-2165 of CBP, which encompass the SRC-1 interacting domain of CBP; FIG. 7e). A GST-CBP fusion protein was expressed in *E. coli* and used for pull-down assays with *in vitro* translated TIF2 polypeptides (FIG. 7d). TIF2 did interact with CBP and, interestingly, the CBP-interacting domain (CID) apparently overlapped the AD1 activation domain of TIF2 (compare FIGS. 7a, c and d; mutants TIF2.8 and TIF2.12). The interaction of TIF2 with CBP was direct, as a purified E. coli-expressed TIF2.1 protein also interacted with GST-CBP (data not shown). Only this region of TIF2 interacted significantly with the GST CBP fusion protein, thus suggesting that the TIF2 AD1 activity may originate from the recruitment of CBP. Purger N-terminal regions (FIGS. 7a and d; mutants TIF2.10 and TIF2.4) or the C-terminal AD2 activation domain (FIGS. 7a and d; mutant TIF2.2) did not show any binding to GST-CBP. Note that TIF2.2 also did not interact win full-length CBP (data not shown), suggesting that the activity of TIF2 AD is mediated by (a) factor(s) distinct from CBP.

To investigate whether the CID of TIF2 could be separated from the AD1 activation domain, the ability of a series of GAL-TIF2 truncation mutants to activate a GAL4-reporter was compared with their ability to interact with the GST-CBP protein *in vitro* (FIG. 9). TIF2.13 (which encompasses Pro_{1011} to Ser_{1122}) exhibited a potent transcriptional activity, comparable to that of larger TIF2 fragments (compare FIGS. 7 and 9). Removal of 26 C-terminal (TIF2.15) or 20 N-terminal (TIF2.18) amino acid residues reduced transcriptional activity only weakly (FIGS. 9a and b). Note that TIF2.13 also interacted with CBP *in vivo*, as shown by using a two hybrid assay in transfected mammalian cells (FIG. 10b).

While the internal deletion of residues Asp_{1061} to Ala_{1070} (TIF2.19) had only a minor effect on the ability of TIF2.13 to transactivate, deletion of the Glu_{1071} to

Leu_{1080} segment (mutant TIF2.20) significantly reduced TIF2 AD1 transcriptional activity. Notably, these residues belong to a sequence predicted to fold into an amphipathic α-helical structure which is highly conserved between TIF2 and SRC-1 (FIG. 9a). The involvement of this region in transactivation was confirmed by analysis of mutants TIF2.21 to TIF2.32 (FIGS. 9a and b). All constructs containing the TIF2 wild-type sequence from Asp_{1075} to Leu_{1087} stimulated transcription, whereas even a deletion of only some of these residues significantly reduced transcriptional activation. However, on its own this α-helical peptide transactivated very poorly, and had to be incorporated into additional upstream and/or downstream TIF2 sequences to generate significant transcriptional activity (FIGS. 9a and b; compare mutants TIF2.13, TIF2.21 and TIF2.32). Importantly, in all cases ADD activity coincided with CBP interaction, since transcriptionally inactive constructs did not interact with CBP (TIF2.24, TIF2.27 and TIF2.29 in FIGS. 9a-c), while transcriptionally active mutants also bound CBP. Moreover, the strength of the *in vitro* interaction with GST-CBP apparently correlated with transactivation efficiency (FIGS. 9a-c; e.g., compare TIF2.21 and TIF2.31).

To investigate whether the integrity of the putative amphipathic α-helical region is required for both AD1 transcriptional activity and interaction with CBP, we introduced point mutations into TIF2.13; the three conserved hydrophobic Leu or the hydrophilic Asp-Glu residues were converted to alanines [FIG. 9a; TIF2.13(LLL) and TIF2.13(DQ)]. Interestingly, mutation of the three leucine residues almost completely abolished AD1 activity, whereas mutation of the Asp-Glu sequence had very little, if any effect (FIG. 10a). Again, AD1 activity and interaction with CBP *in vitro* (FIG. 10c), as well as *in vivo* (FIG. 10b), were strictly correlated, since GAL-TIF2.13(DQ), which transactivated as efficiently as wild type GAL-TIF2.13, interacted strongly with CBP, whereas the transcriptionally inactive GAL-TIF2.13(LLL) interacted very weakly with CBP. Together these results indicate that (i) CBP mediates the AD1 activity of TIF2, (ii) a putative amphipathic α-helix motif located within the AD1 domain is critically involved in, but not sufficient for, efficient CBP binding/transactivation

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and (iii) the amphiphilicity of this motif is not required for AD1 activity and CBP binding.

The two TIF2 activation functions AD1 and AD2 apparently operate through different transcriptional activation cascades. While the TIF2 AD1 activation domain could not be separated by mutational analysis from the TIF2 domain which interacts *in vitro* and *in vivo* with a region of the CBP surface which also mediates SRC-1 binding (Kamei, Y. *et al.*, *Cell 85*:403-414 (1996)), neither this region, nor full length CBP, interacted with TIF2 AD2. That the two TIF2 activation functions may operate through distinct pathways is also suggested by the differential cell specificity of the minimal fragments exhibiting AD1 activity (e.g., TIF2.8, TIF2.7, TIF2.9, TIF2.12) and AD2 activity (TIF2.2). While TIF2.2 is more active in Cos-1 than in HeLa cells, all of the minimal fragments containing AD1 are more active in HeLa cells. Along the same lines, removal in TIF2.3 of sequences N-terminal of TIF2.8 resulted in a 10-fold and 2-fold increased transactivation in Hela and Cos-1 cells, respectively, and removal in TIF2.1 of sequences C-terminal of TIF2.3 gave a 9-fold and 3-fold higher transactivation in Hela and Cos-1 cells, respectively. This suggests that the deleted sequences could exert either intra- or intermolecular repression on TIF2 AD1 activity/CBP interaction. In addition, the coactivator activity of TIF2 may be cell-specifically modulated by the differential efficiency of its two ADs and factors interacting with the sequences N- and C-terminally of the AD1 activation function.

It is worth noting that the core of AD1 (TIF2.32) on its own is a very poor transactivator and CBP binder, and requires additional surrounding sequences to generate a fully active (i.e., efficient CPB binding) surface. However, mutational analysis of the AD1 core in the context of a strong activator fragment (TIF2.13) reveals the critical importance for transactivation and CBP binding *in vivo* and *in vitro* of three leucine residues (FIG. 10). These leucines belong to a conserved LLxxLxxxL (SEQ ID NO:14) motif in all three members of the TIF2 coactivator family (FIG. 9a; Torchia, J. *et al.*, *Nature 387*:677-684 (1987)) which is distinct from the LxxLL (SEQ ID NO:12) NR box motif. Notably, although these

leucines are embedded in a predicted amphipathic α-helix, the amphiphilicity is not required for function, since a mutation of the hydrophilic residues (compare TIF2.13 with TIF2.13 (DQ)) does not affect transactivation/CBP binding.

TIF2 can apparently fulfill at least two mediator functions, (i) as a "bridging factor" between the AF-2 function of nuclear receptors and CBP via its AD1 activation domain and (ii) as a transcriptional mediator through as yet unknown CBP binding-independent route(s) via its AD2 function. Presently, we have no evidence that TIF2 could possess an intrinsic enzymatic activity; none of the bacterially-expressed purified TIF2 fragments, in particular TIF2.1 which was shown to be fully competent in NR and CBP interactions *in vitro*, exhibited any histone acetylase activity under conditions where bacterially-expressed purified yeast GCN5 was highly active (our unpublished results).

Example 6: TIF2 enhancement of NR AF-2 activity

The observation that animal transcriptional activators, such as the human ER (Metzger, D. *et al., Nature 334*:31-36 (1988)), are also active in the yeast *Saccharomyces cerevisiae* demonstrated that the basic principles of transcriptional enhancement have been conserved from yeast to man. We therefore investigated whether TIF2 could enhance transcriptional activation by various NR constructs expressed in *S. cerevisiae*. Both, NRs and TIF2.1 were expressed from multicopy plasmids in the yeast strain PL3(α), which contains a URA3 reporter gene under the control of three estrogen response elements ($(ERE)_3$-URA3; Pierrat, B. *et al., Gene 119*:237-245 (1992)).

In yeast, the hERα constructs were expressed from the following YEp90-based plasmids: HEGO (hERα, YEp90-HEG0, amino acids 1-595), HE15 (YEp90-HE15, amino acids 1-282), and HEG19 (YEp90-HEG19, amino acids 179-595) (all Pierrat, B. *et al., Gene 119*:237-245 (1992)), HE179-338 (YEp90-HE179-338; Pierrat, B. *et al., Gene 143*:193-200 (1994)). From the yeast multicopy plasmid pBL1 (LeDouarin, B. *et al., Nucleic Acids Res. 23*:876-878

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(1995b)), which codes for ER(F)-epitope-tagged ER(C)-fusions, the following plasmids were expressed: ER(C)-RAR(DEF) (pBL1-hRARα(DEF), amino acids 154-462) and ER(C)-RXR(DE) (pBL1-mRXRα(DE), amino acids 205-467) (both vom Baur, E. *et al., EMBO J. 15*:110-124 (1996)). TIF2 was expressed in yeast from the multicopy plasmid pAS3 (gift from B.LeDouann), which is a derivative of YEp90 containing the *LEU2* marker. Yeast PL3(α) (Pierrat, B. *et al., Gene 119*:237-245 (1992)) transformants were grown exponentially in the presence or absence of ligand for about five generations in selective medium containing uracil. Yeast extracts were prepared and assayed for OMP decase activity as described previously (Pierrat, B. *et al., Gene 119*:237-245 (1992)).

As expected from previous studies (Metzger, *Nucl. Acids Res.* (1992); Pierrat, B. *et al., Gene 119*:237-245 (1992); Pierrat, B. *et al., Gene 143*:193-200 (1994)) the full length ER (HEG0) induced orotidine 5'-monophosphate decarboxylase (OMP Decase) activity in a ligand-dependent manner (FIG. 11, lanes 1 and 3). Interestingly, the transcriptional activity of ER was further enhanced by coexpression of the TIF2.1 fragment (FIG. 11, compare lanes 3 and 4). In the absence of hormone, TIF2.1 had no significant effect on ER-induced transcriptional activation (FIG. 11, compare lanes 1 and 2). Essentially the same results were observed for HEG19 which is devoid of the N-terminal region A/B, indicating that TIF2 exerts its effect on the ligand-dependent ER AF-2 (FIG. 11, lanes 5-8). In contrast, neither the AF-1 activity of HE15, (which encompasses the ER regions A, B and C; Kumar & Chambon, *Cell 55*:145-156 (1988)), nor the AF-2a activity of the HE179-338 construct (Pierrat, B. *et al., Gene 143*:193-200 (1994)) were stimulated by coexpressing TIF2.1 (FIG. 11, lanes 9-12). This is in agreement with the results obtained in mammalian cells, and with the observation that an intact LBD is required for TIF2.1 to interact with the ER (Voegel, J.J. *et al., EMBO J. 15*:3667-3675 (1996)).

TIF2.1 also stimulated the AF-2 activity of the liganded RXRα(DEF) region in yeast (FIG. 11, compare lanes 19 and 20). This enhancement was ligand-dependent; no activation via the RXRα(DEF) region was observed when

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the ER(C)-RXRα(DEF) chimera was coexpressed with TIF2.1 in the absence of ligand (FIG. 11, compare lanes 18 and 20). Again these observations parallel those made in HeLa and Cos-1 cells (see FIG. 12c).

Surprisingly, even in the absence of ligand, and in contrast with the observations made with ER and RXRα, TIF2.1 very efficiently enhanced transactivation by the RARα LBD (FIG. 11, lanes 13 and 14). The addition of retinoic acid further increased this transcriptional activation (FIG. 11, lanes 14 and 16). Note that, as previously reported (Heery, D.M. *et al., Nature 387*:733-736 (1997)), both RARα and RXRα AF-2 on their own poorly activated transcription from the URA3 reporter.

The enhancement of AF-2 activity which was particularly strong in yeast cells, has also been recently observed for GRIP1, the mouse homologue of TIF2 (Hong, H. *et al., Mol. Cell. Biol.* 17:2735-2744 (1997)). These observations suggest that yeast cells contain coactivators which only poorly mimic the action of the mammalian NR coactivators. As yeast cells apparently do not contain a CBP homologue, it will be interesting to investigate which yeast factor mediates the activity of TIF2. Note in this respect that GAL-TIF2.1 is a strong transactivator in yeast (our unpublished results).

Interestingly, the expression of TIF2 in yeast led to a marked stimulation of transactivation by the unliganded ER(C)-RARα(DEF), which was not observed with ER or RXRα unliganded LBDs. Structural studies have revealed that binding of the ligand results in a conformational change of the LBD, which generates the surface(s) for coactivator binding (Renaud, J.P. *et al., Nature 378*:681-689 (1995)). Our present result, therefore, suggests that a high level of coactivators might in the absence of ligand drive the LBD of some receptors into a holo-LBD-like conformation, thus giving rise to ligand-independent transcriptional activity. By analogy, one could speculate that high levels of corepressors could "lock" NR LBDs in the apo-LBD conformation. It would therefore be interesting to investigate whether levels of coregulators might lead

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to constitutive activity (even in the presence of antagonists) or conversely to lack of inducibility of nuclear receptors in some pathological states.

Example 7: TIF2 NID inhibition of NR AF-2 activity

Overexpression of the TIF2.1 fragment, which contains both the NID and AD1 activation function, stimulates the ER AF-2 activity of the ER LBD transiently in Cos-1 cells (FIG. 12a, lanes 2 and 3; Voegel, J.J. *et al., EMBO J. 15*:3667-3675 (1996)). That this stimulation was due to a direct interaction between the ER LBD and the NID of TIF2, was strongly suggested by the observation that overexpression of the TIF2.5 mutant which contains the isolated NID, but lacks AD1 (see FIG. 7a) prevented the stimulatory effect of TIF2.1 (FIG. 12a, compare lanes 3 and 4). Note that in the absence of TIF2.1, TIF2.5 overexpression also decreased the transactivation by the ER AF-2 which was presumably mediated through Cos-1 endogenous coactivators (FIG. 12a, compare lane 4 with lane 2), thus suggesting that these Cos-1 mediators either correspond to endogenous TIF2s, or interact with the ER holo-LBD through surfaces which are identical to, or in direct vicinity of, the TIF2 NID interaction surface.

We previously reported an agonist-dependent interaction of TIF2 with RAR and RXR LBDs, which was dependent on the integrity of the NR AF-2 AD core, but failed to observe a stimulatory effect of TIF2 on the transcription activation of a $(17m)_5$-Globin-promoter-CAT reporter by GAL-RAR LBD or GAL-RXR LBD fusion proteins (Voegel, J.J. *et al., EMBO J. 15*:3667-3675 (1996)). Since this failure was likely to be due to the presence of sufficient amounts of endogenous mediators for achieving maximal transactivation from this reporter gene, we modified the transfection conditions and used a reporter construct bearing a minimal promoter. A clear TIF2 and TIF2.1 stimulatory activity for RXRα AF2 was observed in HeLa and Cos-1 cells when using the $(17m)_5$-TATA-CAT reporter (FIG. 12c, compare lanes 3-6 and 11-14). This stimulatory effect was less marked with RARα AF-2 and could be observed

reproducibly only with the TIF2.1 fragment in Cos-1 cells (FIG. 12d, compare lane 10 with lanes 13 and 14; note that TIF2.1 is expressed at >10 fold higher levels than TIF2; data not shown). The reporter plasmids $(17m)_5$-TATA-CAT (May, M. *et al.*, *EMBO J. 15*:3093-3104 (1996)) and 17M5-G/CAT ($(17m)_5$-β-globin-CAT; Durand, B. *et al.*, *EMBO J. 13*:5370-5382 (1994)) each contain five copies of the GAL4 response element in front of a simple TATA motif or of the β-globin promoter, respectively, upstream from the CAT reporter gene.

Assuming that TIF2 or coactivators recognizing the TIF2 interacting surface on NR LBDs, generally mediate the AF-2 function of NRs, the NID containing TIF2.5 should exert its dominant negative activity not only on ER, but also on other NRs, independently of the cellular context. We therefore analyzed the effect of TIF2.5 on the AF-2 activity of ER, RXRα and RARα in HeLa and in Cos-1 cells (FIGS. 12b-d). In all cases, TIF2.5 expression led to a dose-dependent inhibition of the NR AF-2 activity, indicating that the endogenously present mediators were competed out by the isolated overexpressed TIF2 NID, and strongly suggesting that TIF2 or transcriptional intermediary factors recognizing the same or overlapping surfaces mediate NR AF-2 activity in these transfected cells (FIGS. 12b-d, compare lane 2 with lanes 7 and 8; lane 10 with lanes 15 and 16).

It is important to stress that our present data demonstrate that TIF2 interacts with NRs through a surface (NID) that is critical for NR AF-2 activity, as expression of TIF2.5 which encompasses the NID blocked the ligand-induced activity of all tested NR AF-2s. This observation which clearly establishes that, at least in transfected cells, TIF2 or other coactivators which interact with an overlapping, if not identical, holo-LBD surface, are essential to mediate the NR AF-2 activation function. This is in keeping with the presence of three NR box motifs in the TIF2 NID, and of at least one conserved LxxLL (SEQ ID NO:12) NR box motif in all coactivators described to date.

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It will be apparent to those skilled in the art that various modifications and variations can be made in the methods of the present invention without departing from the spirit and scope of the invention. Thus, it is intended that the present invention cover all modifications and variations of this invention provided they come within the scope of the appended claims and their equivalents.

The disclosures of all patents, patent applications, and publications referred to above are hereby entirely and expressly incorporated herein by reference.

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